

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:22:24 ; Search time 6020 Seconds
(without alignments)
10622.738 Million cell updates/sec

Title: US-10-647-649-2

Perfect score: 1125

Sequence: 1 ttcatggcagctcagcacat.....ctaattaaactataaata 1125

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5881141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	431.4	38.3	1296	15 AK104862	AK104862 Oryza sat
3	431.2	38.3	993	6 AX53028	AX53028 Sequence
4	430.6	38.3	1141	15 AF001523	AF001523 Musa acum
5	430	38.2	1261	6 AX006978	AX006978 Sequence
6	427.2	38.0	1439	15 AF112967	AF112967 Triticum
7	423.2	37.6	110000	15 AP008207	Continuation (414
8	423.2	37.6	164394	15 AP004031	AP004031 Oryza sat
9	422	37.5	1426	15 TABE7GLUB	Z22874 T.aestivum
10	421.8	37.5	1041	15 AF004838	AF004838 Musa acum
11	419.4	37.3	1295	15 AK070677	AK070677 Oryza sat
12	418.2	37.2	1834	15 OSU72251	U72251 Oryza sativ
13	415.6	36.9	3559	6 BD080855	BD080855 Banana pr
14	409.8	36.4	1249	15 AY612193	AY612193 Hordeum v
15	394.2	35.0	1434	15 TABE7GLUA	Z22873 T.aestivum
16	393.6	35.0	1448	15 ASBGJUCAN	Z15131 A.sativa mr
17	382.4	34.0	6260	15 HVBDG	X52572 Barley DNA
18	380.8	33.8	4643	15 HVGLUB2	X56260 Barley DNA

19	380.8	33.8	4849	15 HVGLB1	X56775 H.vulgare G
20	378.6	33.7	5159	15 BLYGLB2	M62740 Hordeum vul
21	370.2	32.9	1265	15 MZEL1BGLCN	M95407 Wuglu; Zea
22	368.2	32.7	1269	15 AF112965	AF112965 Triticum
23	364.8	32.4	1311	15 AY353062	AY353062 Vitis rip
24	360	32.0	874	15 BLYGLUCB	M13237 Barley beta
25	357.6	31.8	1243	15 S82315	S82315 PRm 6b-1.3-
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36	346.2	30.8	1235	6 AR164399	AR164399 Sequence
37	346.2	30.8	1235	6 I75201	I75201 Sequence 11
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39	343.4	30.5	1245	15 AK068247	AK068247 Oryza sat
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43	341.6	30.4	1250	15 BLYGRH	M23548 Hordeum vul
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ALIGNMENTS

RESULT 1

AB027428

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

REFERENCE

AUTHORS

JOURNAL

FEATURES

source

CDs

AB027428 Oryza sativa mRNA for beta 1,3-glucanase, complete cds,
clone: E1149.

AB027428.1 GI:4884525
Oryza sativa beta 1,3-glucanase.

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 1280)
Itoh, Y. and Sasaki, T.
Oryza sativa mRNA for beta 1,3-glucanase
Published Only in Database (1999)

2 (bases 1 to 1280)
Itoh, Y. and Sasaki, T.
Direct Submission
Submitted (17-MAY-1999) Yoshifumi Itoh, National Food Research
Institute, Applied Microbiology; Kannondai 2-1-2, Tsukuba, Ibaraki
305-8642, Japan (E-mail: yosifumi@nri.affrc.go.jp,
Tel: +81-298-38-8075, Fax: +81-298-38-7996)

Location/Qualifiers
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ORIGIN

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DB |||||
QY 146 GCCATTCTACAGTGGTCAATCTATCGCGTGTCTACGGCGTGTATCGGGAACAACCTG 205
DB |||||
QY 124 CCCAGCGCGGAGCTGTCACTCTACAGTCTCAACATCAACATAGCTGGCATGGAGCTC 183
DB |||||
QY 206 CGGTGCGGAGCGAGCTGTGCGAGCTCTACAAGTCCAAACGGCATCGACTCCATGGGCATC 265
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QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGCGCTTAACATCTACTCTCATCTC 243
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QY 244 GACGTCCCAACTCCGACCTCCAAACATTTGCTCCGACCAATCCGCGCCGACCAACTGG 303
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DB |||||
QY 731 CCGGCGACGGTGGTTCAGAGCGCGGCAACCGGTACCAAGAACCTGTTTCGAGCGCCATCGTC 790
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QY 791 GACAGTTTCTACTCGCGCTGGAGAGCGCGGCGCGGAGCGTCCCGATCGTGGTGTGTCG 850
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QY 784 GAGAGTGGTGGCGCTCAGCGCGCGGAGCAGCGGCGAGCGGTGCTCTAAATGCGCAGACTTAC 843
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QY 851 GAGAGCGGTGGCTCTCGCGCGCGGACGCGGCGGCGGCGGCGGCAACGCGCAGAGCTAC 910
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QY 904 ACCTACATATTTCGATGCTTCAACAGGATCAGAAAGCAGCCGCAAGGATTTGAGATAAC 963
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QY 964 TTTCGGCTGTTTTTACCCTTAACGACGCTCTTATTCGATCAGCTTCACTTTGAGAAAT 1023
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QY 1024 T 1024

DB 1091 T 1091

RESULT 2

AKI04862

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) cDNA clone:001-043-E09, full

insert sequence.

AKI04862

ACCESSION

AKI04862.1 GI:32990071

VERSION

FLI_CDNA; oligo capping.

KEYWORDS

Oryza sativa (japonica cultivar-group)

SOURCE

Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1

The Rice Full-Length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-Length cDNA Project Team;

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,

Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,

Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,

Ohtsuki,K., Shishiki,T., Foundation of Advancement of International

Science Genome Sequencing & Analysis Group; Otonoda,Y.,

Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,

Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,

Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,

Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,

Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;

Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,

Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Oato,N., Oka,Y.,

Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Yoshino,M. and Hayashizaki,Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

12869764

2 (bases 1 to 1296)

ADACHI,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,

Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Haseizume,W.,

Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,

Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,

Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,

Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,

Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,

Koda,T., Kojima,K., Kojima,Y., Kondo,S., Komono,H., Kouda,M.,

Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,

Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,

Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,

Naniki,T., Nariawa,R., Niikura,J., Nishi,K., Nomura,K.,

Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,

Osato,N., Ota,Y., Otonoda,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,

Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,

Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,

Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,

Tagawa,A., Takahashi,P., Takaku-Akaira,S., Tanaka,T., Tomaru,A.,

Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,

Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and

Yoshimura,A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of

Agrobiological Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skkuchikuchi@affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

COMMENT

URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narioka, R., Niihara, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsuura, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

source

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ORIGIN

Query Match 38.3%; Score 431.4; DB 15; Length 1296;
Best Local Similarity 66.8%; Pred. No. 3.4e-75;
Matches 682; Conservative 0; Mismatches 321; Indels 18; Gaps 4;
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102 ATGGCAAGCATGGGTGCTTCCGTTTAACTGAGTGGATGGTCTCTTGGAG---TTGCG 158
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RESULT 3
AX653028
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DEFINITION Sequence 2898 from Patent WO0300098.
ACCESSION AX653028
VERSION AX653028.1 GI:29155842
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 0300098-A 2898 03-JAN-2003;
Syngenta Participations AG (CH)
FEATURES
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ORIGIN

Query Match 38.3%; Score 431.2; DB 6; Length 993;
Best Local Similarity 67.2%; Pred. No. 3.7e-75;
Matches 677; Conservative 0; Mismatches 313; Indels 18; Gaps 4;

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RESULT 4
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LOCUS Musa acuminata beta-1, 3-glucanase mRNA, complete cds.
DEFINITION

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AF001523
AF001523.2 GI:6073859
Musa acuminata
Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE
1 (bases 1 to 1141)
Clendennen,S.K. and May,G.D.
Differential gene expression in ripening banana fruit
Plant Physiol. 115 (2), 463-469 (1997)
9342866
2 (bases 1 to 1141)
Peumans,W.J., Barre,A., Derycke,V., Rouge,P., Zhang,W., May,G.D.,
Delcour,J.A., Van Leuven,F. and Van Damme,E.J.
Purification, characterization and structural analysis of an
abundant beta-1,3-glucanase from banana fruit
Eur. J. Biochem. 267 (4), 1188-1195 (2000)
10672030
3 (bases 1 to 1141)
Clendennen,S.K. and May,G.D.
Direct Submission
Submitted (29-APR-1997) Plants and Human Health, Boyce Thompson
Institute for Plant Research, Tower Rd., Ithaca, NY 14853, USA
4 (bases 1 to 1141)
Van Damme,E.J., May,G.D. and Clendennen,S.K.
Direct Submission
Submitted (20-OCT-1999) Lab. Phytopathology and Plant Protection,
K. U. Leuven, Willem de Croylaan 42, Leuven B 3001, Belgium
Sequence update by submitter
On Oct 20, 1999 this sequence version replaced gi:2586138.
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Best Local Similarity 67.0%; Pred. No. 4.8e-75;
Matches 706; Conservative 0; Mismatches 329; Indels 18; Gaps 6;
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QY 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGGTCTGCAATGGAATGGAGCGGTGACAACTTC 123
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61 GCAGTTCCACAAGAGTGCATTCGATTGGTCTGCTACGCGATGCTCGGCAACAATCTT 120
QY 124 CCCAGCCCGGAGCGCTGTCACCTCTACAAGTCCCAACACATAGCTGGCATCGGACTC 183
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121 CCCCAGCCCGAGCGAGTGGTCAGTCTCTACAAATCCCAACAATCGCGAGATGAGACTC 180
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGCTCTTAACATCTACTCTATCTC 243
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181 TACGATCCAAACCAAGCGCGCTCGAAGCCCTCAGGAACCTCAACATCCCAAGTCTCTGTTG 240
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Qy	655	TTTACTGCACTCTGGTACAGTTCGTACAGACGGGTCTACGGCTTACAAACAACCTCTTCGAT	714
Db	685	TTTTACTTCCCGGGACTGTAGTGACAGATGGACAATATAATATCAGAACCTCTTTGAT	744
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Qy	775	GTCTGTCTGGAGAGTGGCTTGGCCGTTCAGCGGCGGGACAGCGGCACGGTGTCTAATCGG	834
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Qy	835	CAGACTTACAATTCGAATTTTGATCAACCAATGTGGGTTCAGGGGACCGCGAAGAGGCCAGG	893
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Qy	894	--GGCGATTGAGACCTTACATATTTGGCCATGTTCAACGAGGATCAGAAGCAGCGCAAGGG	951
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Qy	952	ATTGAGAATAACTTTGGGCTGTTTTACCTTAAAGAACAGCGCTGCTCTATTTCGATCAGCTTC	1011
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RESULT 6	AF112967	1439 bp	mRNA	linear	PLN 06-MAY-2002
LOCUS	AF112967				
DEFINITION	Triticum aestivum beta-1,3-glucanase precursor (Glb3) mRNA, complete cds.				
ACCESSION	AF112967				
VERSION	AF112967.1	GI:4741849			
KEYWORDS	.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	1 (bases 1 to 1439)				
AUTHORS	Li, W., Faris, J.D., Muthukrishnan, S., Liu, D., Chen, P. and Gill, B.S.				
TITLE	Isolation and Characterization of cDNA Clones of Acidic Chitinases and beta-1,3-Glucanases from Wheat Spike Induced by Fusarium graminearum				
JOURNAL	Theor. Appl. Genet. 102, 353-362 (2001)				
REFERENCE	2 (bases 1 to 1439)				
AUTHORS	Li, W., Faris, J.D., Muthukrishnan, S., Liu, D., Chen, P. and Gill, B.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-DEC-1998) Department of Plant Pathology, Kansas State University, St. Claiflin, Manhattan, KS 66506-5502, USA				
FEATURES	Location/Qualifiers				
source	1. .1439				

ORIGIN

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Qy	81	GGAAATCATTTGGGGTCTGCAATGGAAATGGAGCGGTGAACAACCTCCCGACGCCCGCGACGT	140
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Qy	201	CACCTCTCCAGGCGCTCCAGGGCTTTAACTACTACCTCATCTCGAGCTGCCCAACTCCGA	260
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AP008207_001	100001 210000
AP008207_002	200001 310000

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Qy 253	AACTCGAACCTCCAAAACATTGCTCCGACCAATCCGCGGCCACCAACTGGGTCCAAACC 312		
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Qy 553	ATACAGTTTCTAGCCAGCAATGGCTCCGCCATTCTGCCAACATCTACCCCTACTTTGAGC 612		
Db 40069	GCTCAGTACCTGGGAGGACCGGCGCGCGTGTTCGCCAAGCTCTACCCCTACTTCGCC 40128		
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DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,			
PAC clone: P0432C03.			
ACCESSION AP004031 BA000010			
VERSION AP004031.3 GI:18844943			
KEYWORDS			
SOURCE			
ORGANISM			
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Oryza sativa (japonica cultivar-group)			
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
Ehrhartoideae; Oryzeae; Oryza.			
1			
REFERENCE			
AUTHORS			
Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,			
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,			
Antonio, B. A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,			
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,			
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,			
Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, Y.,			
Ikuta, A., Kobayashi, N., Kono, I., Machita, K., Maehara, T.,			
Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,			
Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,			
Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,			
Shomura, A., Song, J., Takasaki, Y., Terasawa, K., Tsuji, K., Waki, K.,			
Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,			
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,			

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QY 1005 TGGGACTCTTCTACCCCAACATGCGACGCTTACCCCATCAGCTTCTGATGAGTAGC 1064
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DEFINITION
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ACCESSION
AF004838
VERSION
AF004838.1 GI:6448756
KEYWORDS
Musa acuminata
SOURCE
Musa acuminata
ORGANISM
Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Musa.
REFERENCE
1 (bases 1 to 1041)
Chen, Y.-C., Do, Y.-Y. and Huang, P.-L.
Isolation and nucleotide sequence of a fruit ripening-related cDNA
encoding glucan endo-1,3-beta-glucosidase homolog from banana
(Accession No. AF004838) [FGR97-151]
Plant Physiol. 115 (2), 864 (1997)
REFERENCE
2 (bases 1 to 1041)
Huang, P.
Direct Submission
Submitted (20-MAY-1997) Horticulture, National Taiwan University,
No.1 Section 4 Roosevelt Road, Taipei, Taiwan 10617, Republic of
China
FEATURES
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Db |||||
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LOCUS AK070677 1295 bp mRNA linear PLN 24-JUL-2003
DEFINITION *Oryza sativa* (japonica cultivar-group) cDNA clone.J023063017, full insert sequence.
ACCESSION AK070677
VERSION AK070677.1 GI:32980701
KEYWORDS FLI CDNA; CAP trapper.
SOURCE *Oryza sativa* (japonica cultivar-group)

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; *Oryza*.

REFERENCE

AUTHORS

The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, H., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ohtsuki, K., Itoh, M.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kuroesaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
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Yoshino, M. and Hayashizaki, Y.

TITLE

Japonica rice
Science 301 (5631), 376-379 (2003)

JOURNAL

PUBMED

REFERENCE

AUTHORS

2 (bases 1 to 1295)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
Hori, F., Hotta, I., Iida, Y., Ikeda, R., Imamura, K.,
Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kuroesaki, T., Kusumegi, T., Li, C., Lu, M.,
Koya, S., Kurihara, C., Kurosaki, T., Matsuyama, T., Miura, J., Miyazaki, A.,
Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M.,
Mizuno, K., Murakami, K., Niikura, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
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Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tegawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.

Direct Submission

Submitted (05-DSC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel: 81-29-838-7007, Fax: 81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>

NTAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
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Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
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Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

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Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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LOCUS
DEFINITION
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Oryza sativa beta-1,3-glucanase precursor (Gns5) gene, complete cds.
ACCESSION
U72251
VERSION
U72251.1 GI:4097939
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Oryza sativa (japonica cultivar-group)
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REFERENCE
1 (bases 1 to 1834)
Romer, G.O., Simmons, C., Yaneshita, M., Doan, M., Thomas, B.R. and
Rodriguez, R.L.
Characterization of rice endo-beta-glucanase genes (Gns2-Gns14)
defines a new subgroup within the gene family
Gene 223 (1-2), 311-320 (1998)
JOURNAL
PUBMED
9858757
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2 (bases 1 to 1834)
Romer, G.O., Simmons, C.R. and Rodriguez, R.L.
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TITLE
Submitted (24-SEP-1996) Molecular and Cellular Biology, University
of California at Davis, Davis, CA 95616, USA
JOURNAL
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VERSION		fruit development.
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ORGANISM		Musa acuminata
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AUTHORS		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE		Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
JOURNAL		Musa.
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ACCESSION AY612193
VERSION AY612193.1 GI:51860172
KEYWORDS
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REFERENCE
AUTHORS Troedson, U., Green, B., Widell, S., Collinge, D. and Bryngelsson, T.
TITLE Isolation and characterization of three beta-1,3 glucanases from
barley leaves (Hordeum vulgare, L.) infected by the powdery mildew
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JOURNAL Unpublished
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REFERENCE
AUTHORS Troedson, U., Green, B., Widell, S., Collinge, D. and Bryngelsson, T.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2004) Cell and Organism Biology, Solvegatan 35B,
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Location/Qualifiers
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Db CGAATAATCGCGGCGCTTACCCCATCAGTTTC 1054

RESULT 15
TABETGLUA
LOCUS TABETGLUA 1434 bp mRNA linear PLN 18-APR-2005
DEFINITION T.aestivum beta glucanase mRNA, complete CDS.
ACCESSION Z22873
VERSION Z22873.1 GI:311705
KEYWORDS beta glucanase.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 111 to 1434)
Lai,D.M., Hoj,P.B. and Fincher,G.B.
Purification and characterization of (1->3, 1->4)-beta-glucan
endohydrolases from germinated wheat (*Triticum aestivum*)
Plant Mol. Biol. 22 (5), 847-859 (1993)
JOURNAL 8358032
REFERENCE 2 (bases 1 to 1434)
Fincher,G.B.
Direct Submission
Submitted (01-JUN-1993) Fincher G. B., University of Adelaide,
Waite Campus, Plant Science, Glen Osmond, South Australia,
Australia, 5064
FEATURES
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/evidence=experimental
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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Result	
No.	Score	Query Match	Length DB ID	Description	
1	1125	100.0	1125 14	ADY53162	
2	431.2	38.3	993 8	ADA69575	Ady53162 Lily beta
3	430	38.2	1261 3	AAZ50051	Ada69575 Rice gene
4	427.2	38.0	1439 13	ADT19801	Aaz50051 Mesocarp
5	426.4	37.9	993 2	AAZ33567	Adt19801 Plant CDN
6	418.2	37.2	1834 2	AAZ33533	Aax33567 Rice Gns5
7	415.6	36.9	3559 2	AAZ25612	Aax33533 Rice beta
8	411.2	36.3	912 2	AAZ33557	Aax25612 Banana ri
9	408.6	36.3	1463 2	AAQ24291	Aax33557 Rice beta
10	394.2	35.0	1458 13	ADT19681	Aaq24291 (1-3,1-4)
11	393.6	35.0	1257 2	AAQ24292	Adt19681 Plant CDN
12	381.6	33.9	1268 13	ADX51668	Aaq24292 (1-3,1-4)
13	380.8	33.8	4643 3	AAQ24290	Adx51668 Plant ful
14	380.8	33.8	4849 10	ADL18243	Aaq24290 (1-3,1-4)
15	354.2	31.5	1110 11	ADJ11803	Adl18243 Barley ge
16	353.8	31.4	1113 11	ADJ11469	Adj11803 Rice CDNA
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21	334.8	29.8	972	11	ADJ11685	Adj11685 Rice DNA
22	334.4	29.7	957	8	ADA71217	Ada71217 Rice gene
23	334.4	29.7	1212	14	AEb66698	Aeb66698 Rice geno
24	334.4	29.7	1212	14	AEb67682	Aeb67682 Rice geno
25	330.6	29.4	996	2	AAZ33568	Aax33568 Rice Gns6
26	329.8	29.3	1005	8	ADA69783	Ada69783 Rice gene
27	329.8	29.3	1005	11	ACL30336	Adl30336 Rice abio
28	325.6	28.9	954	11	ADJ11741	Adj11741 Rice cdna
29	325.6	28.9	957	11	ADJ11401	Adj11401 Rice DNA
30	325.2	28.9	1005	8	ADA69785	Ada69785 Rice gene
31	325.2	28.9	1005	11	ACL27113	Adl27113 Rice abio
32	325	28.9	2169	2	AAZ33534	Aax33534 Rice beta
33	319.6	28.4	921	2	AAZ33558	Aax33558 Rice beta
34	319	28.4	1228	13	ADX53559	Adx53559 Plant ful
35	318.6	28.3	1008	2	AAZ33565	Aax33565 Rice Gns3
36	314.6	28.0	1176	14	AEb67100	Aeb67100 Rice geno
37	313.8	27.9	1017	9	ADA48623	Ada48623 Rice gene
38	310	27.6	1949	2	AAZ33531	Aax33531 Rice beta
39	301.6	26.8	1245	13	ADX48400	Adx48400 Plant ful
40	301.6	26.8	1249	13	ADX48460	Adx48460 Plant ful
41	299.2	26.6	1101	9	ADA48291	Ada48291 Rice gene
42	298	26.5	918	2	AAZ33555	Aax33555 Rice beta
43	296	26.3	1261	13	ADX53067	Adx53067 Plant ful
44	295.2	26.2	996	2	AAZ33566	Aax33566 Rice Gns4
45	293.4	26.1	1204	13	ADX60908	Adx60908 Plant ful

ALIGNMENTS

RESULT 1

ADY53162

ID ADY53162 standard; CDNA; 1125 BP.

XX

AC ADY53162;

XX

DT 19-MAY-2005 (first entry)

XX

DE Lily beta-1, 3 glucanase CDNA, LPGLul.

XX

KW Beta-1, 3 glucanase; glucan endo-1, 3 glucan glucanhydrolase;

KW transgenic plant; disease resistance; crop improvement;

KW plant fungal disease; antifungal agent; plant; gene; ss.

XX

OS Liliaceae.

XX

FH Key

FT CDS

FT Location/Qualifiers

FT 4..1017

FT /*tag= a

FT /product= "Lily LPGLul protein"

XX

PN US2005048638-A1.

XX

PD 03-MAR-2005.

XX

PF 26-AUG-2003; 2003US-00647649.

XX

PR 26-AUG-2003; 2003US-00647649.

XX

PA (CHEN/) CHEN C.

PA (HOUP/) HOU P.

XX

PI Chen C, Hou P;

XX

DR WPI; 2005-195288/20.

DR P-PSDB; ADY53161.

XX

PT New nucleic acid sequence encoding beta-1,3-glucanase, useful for

PT producing a transgenic plant with enhanced resistance against fungi.

XX

PS Example 2; SEQ ID NO 2; 14pp; English.

XX

CC The present invention relates to beta-1, 3 glucanase polynucleotide and
CC its encoding polypeptide obtained from lily plant. The invention is
CC useful for producing a transgenic plant with enhanced resistance against
CC a wide variety of stresses particularly fungal attack such as Botrytis
CC blight and gray mold. The polypeptide of the invention is also capable of
CC degrading the cell wall of fungi and thus can be used as an antifungal
CC agent. The present sequence is lily beta-1, 3 glucanase cDNA, LPGA1ul
CC (lily pathogen-induced glucanase 1).

XX SQ Sequence 1125 BP; 272 A; 356 C; 245 G; 252 T; 0 U; 0 Other;

Query Match 100.0%; Score 1125; DB 14; Length 1125;

Best Local Similarity 100.0%; Pred. No. 9.6e-278;

Matches 1125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCTAGCGAGCTCAGACATCATCTCCATGGCTGCCATGGCATCCCTCTTTGTAGTACTC 60
Db 1 TTCTAGCGAGCTCAGACATCATCTCCATGGCTGCCATGGCATCCCTCTTTGTAGTACTC 60
Qy 61 TCGGCATCCCGAGAGGGCTGGATCCATTTGGGTCTGCAATGGATGGACGGTGACAC 120
Db 61 TCGGCATCCCGAGAGGGCTGGATCCATTTGGGTCTGCAATGGATGGACGGTGACAC 120
Qy 121 CTCCCCAGCGCGCGAGCTCGTCAACCTCTACAGTCCAAACAACATAGCTGGCATGCGA 180
Db 121 CTCCCCAGCGCGCGAGCTCGTCAACCTCTACAGTCCAAACAACATAGCTGGCATGCGA 180
Qy 181 CTCTAAGCCCGACCAAGCAGCTCTCCAGGCCCTCCAGGGCTCTTAACATCTACTCATC 240
Db 181 CTCTAAGCCCGACCAAGCAGCTCTCCAGGCCCTCCAGGGCTCTTAACATCTACTCATC 240
Qy 241 CTGACGTCCTCCAACTCGAGCTCCAAACATTGGCTCCGACCAATCCGCGCCACCAAC 300
Db 241 CTGACGTCCTCCAACTCGAGCTCTCAAAACATTGGCTCCGACCAATCCGCGCCACCAAC 300
Qy 301 TGGGTCCAAACCAAGCTCCAAAGCTTACCAAGCTTGGCTCCGATACATCGCGTGGGA 360
Db 301 TGGGTCCAAACCAAGCTCCAAAGCTTACCAAGCTTGGCTCCGATACATCGCGTGGGA 360
Qy 361 AACGAAGTCATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGGCCATGAACAACATACAG 420
Db 361 AACGAAGTCATCCCGCGGCGCAAGCTCAGTACGTCCTCCAGGCCATGAACAACATACAG 420
Qy 421 TCGGCCCTCTCTCTGCGGGCTTCAGAAACATCAAGTCTCCATCAGTCTCTCTTGGC 480
Db 421 TCGGCCCTCTCTCTGCGGGCTTCAGAAACATCAAGTCTCCATCAGTCTCTCTTGGC 480
Qy 481 GTGCTGCTGCTCATATCCCCCTCAGCTGGCTCTCTCTCCGATGCATCGTCGACA 540
Db 481 GTGCTGCTGCTCATATCCCCCTCAGCTGGCTCTCTCTCCGATGCATCGTCGACA 540
Qy 541 TTGGGTCCAATCATAAGTTTCTAGCCAGCAATGGCTCCCATTAATTTGCCAATCTAC 600
Db 541 TTGGGTCCAATCATAAGTTTCTAGCCAGCAATGGCTCCCATTAATTTGCCAATCTAC 600
Qy 601 CCTACTTGAGTATGCTGGCACTCCCGATCCATCGACCTCTCATCGCCCTCTTACT 660
Db 601 CCTACTTGAGTATGCTGGCACTCCCGATCCATCGACCTCTCATCGCCCTCTTACT 660
Qy 661 GCATCTGGTACAGTCTGACAGAGGGTCTTACGCTTCAACAACCTCTTCGATGCCATG 720
Db 661 GCATCTGGTACAGTCTGACAGAGGGTCTTACGCTTCAACAACCTCTTCGATGCCATG 720
Qy 721 GTGACGCAATGTTACTCGGCCCTTGAGAGCGCCGAGGGCCGAATGTCCCTGTTGCTGT 780
Db 721 GTGACGCAATGTTACTCGGCCCTTGAGAGCGCCGAGGGCCGAATGTCCCTGTTGCTGT 780
Qy 781 TCGGAGAGTGGTGGCCCTCAGCGGGCGGACAGCGGGCGAGCGGTCTTAATGCCGAGACT 840
Db 781 TCGGAGAGTGGTGGCCCTCAGCGGGCGGACAGCGGGCGAGCGGTCTTAATGCCGAGACT 840
Qy 841 TACAATTCGAATTTGATCAACCATGTGGGTGAGGGGACCGCGAAGAGCCAGGGGCGGATT 900
Db 841 TACAATTCGAATTTGATCAACCATGTGGGTGAGGGGACCGCGAAGAGCCAGGGGCGGATT 900

Db 841 TACAATTTCCAATTTGATCAACCATGTGGGTGAGGGGACGCGAAGAGCCAGGGCGGATT 900
Qy 901 GAGACCTACATATTTGGCATGTTTCAACGAGGATCAGAAGCAGCCGCAAGGATTTGAGAA 960
Db 901 GAGACCTACATATTTGGCATGTTTCAACGAGGATCAGAAGCAGCCGCAAGGATTTGAGAA 960
Qy 961 AACTTTGGGCTGTTTTACCCCTTAACGACAGCTGCTTATTCGATCAGCTTCACCTTGAGAA 1020
Db 961 AACTTTGGGCTGTTTTACCCCTTAACGACAGCTGCTTATTCGATCAGCTTCACCTTGAGAA 1020
Qy 1021 ATTTGATCAGATGAATATAATAAAGGCTTATATTTGTAAGGCAAGCTTCGTAATTGA 1080
Db 1021 ATTTGATCAGATGAATATAATAAAGGCTTATATTTGTAAGGCAAGCTTCGTAATTGA 1080
Qy 1081 TAGCCATCTAGTATATAGCTTCGGCTAAATTAACCTATATAAATA 1125
Db 1081 TAGCCATCTAGTATATAGCTTCGGCTAAATTAACCTATATAAATA 1125

RESULT 2

ADA69575

ID ADA69575 standard; DNA; 993 BP.

XX ADA69575;

XX 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 2898.

DE Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.

XX Oryza sativa.

OS WO2003000898-A1.

PN 03-JAN-2003.

PD 22-JUN-2001; 2001WO-IB001105.

PF 22-JUN-2001; 2001WO-IB001105.

PR (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX WPI; 2003-175290/17.

DR Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

XX Claim 6; SEQ ID NO 2898; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX Sequence 993 BP; 190 A; 356 C; 285 G; 162 T; 0 U; 0 Other;

Query Match 38.3%; Score 431.2; DB 8; Length 993;

Best Local Similarity 67.2%; Pred. No. 4.9e-100;

Matches 677; Conservative 0; Mismatches 313; Indels 18; Gaps 4;

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QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTGTAGTACTCTCG 63
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ATGGCAAGACATGCGCTGCTCCGTTTAAACATGGCATGTGCTCTTGGAG---TTGG 57
QY 64 GCAATCCCGAGAGCGCTGCAATCCATGGGGTCTGCAATGGATGACGCTGACACCTC 123
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
58 GCATTCCTACAGTGTGCAATCTATCGGGTGTGCTACGGGTGATCGGGAAACCTG 117
QY 124 CCGCAGCCGCGAGCGTCTCAACCTTAAAGTCCAAACAACATAGCTGGCATGCACTC 183
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 CGGTGCGCGAGCGCTGCGAGCTTACAAAGTCCAAAGGCATCGACTCCATGCGCATC 177
QY 184 TACAGCCCGCAGCAAGCACTCTCCAGGCGCTCCAGGCTCTAAATCTACTATCTCTC 243
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
178 TACTTCCCAAGAGGACATCTCTCAGGCGCTCAGCGGCTCAAGCATCGCCCTCCCA 237
QY 244 GACGTCCCCCACTCCGACCTCCAAACATTTGCTCCGACCAATCGCGCCCACTACTGG 303
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
238 GAGTGGGCAACGATCAGTCTGGCTCCCTCGCTCGACCCCTCGCGCCCGCGCTTC 297
QY 304 GTCCAAACCAACGTCCAGCCTACCCAAAGTTGCTTCCGATACATCGCCGTCGGAAC 363
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 GTCCAGAACAACTCAGCGCTTCCGCGCGTCAACTTCCGCTACATCAGGTGCGCAAC 357
QY 364 GAAGTCATCCCGCGGCGCAAGTCACTAGTGTCTTCCAGCCATGAACAACTAGTCC 423
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
358 GAGG---TTTCCGGCGGCGACACGAGAAATCTCTCCCGCCATGCAACATGAACAGC 414
QY 424 GCGCTCTCTCTCGCGGCTTCCAGAACATCAAGGTCTCCACATAGTCTCTTCCGGCTC 483
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
415 GCGCTCTCTCGCGGCTTCCAGAACATCAAGGTCTCCAGGTGTGACGTGGTCTCCAGG 474
QY 484 TTCGCTACTCTATATCCCGCTCAGTGGCTCTCTCTTCCGATGCTATCGACATTTG 543
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
475 ACCG---CGGCTTCCGCGGCTCCGCGGCGACGTTCTCGCC-----TCGCATG 522
QY 544 GTTCAATCATACAGTTTCTAGCAGCAATGCTCCCAATTAATTTGCGCAACATTCACCC 603
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
523 GGGCCCATAGTCTCAGTACCTGGCGAGCACCGCGCGCGCTGCTCGCCAAACGCTTACCC 582
QY 604 TACTTGAGCTATGCTGGCAATCCGATCCATCGACCTCTCATAGCCCTCTTTACTGCA 663
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
583 TACTTGGCTAGCTGGGCAACAGGCCCGAGATCGACATCAACTACGCGCTCTTACGTCG 642
QY 664 TCTGTACAGTGTGACAGAGCGGCTCTACGCTTACAAACCTCTTCGATGCCATGCTC 723
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
643 CCGGSCACGGTGTGACAGAGCGCGGCAACGGGTACAGAACCTGTTGACGCCATGCTC 702
QY 724 GACGATTTGTTACTCGGCGCTGAGAGCGCGGAGCGCGAATGTCCCTGTTGTGCTGTCG 783
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
703 GACAGCTTCTACTCCGCGCTGGAGAGCGCGCGCGCGGAGCGTCCCGATCGTGTGTCG 762
QY 784 GAGAGTGGCTGGCGCTGACGGCGGGGACAGGGCGAGCGGTGCTTAATGCGCAGACTTAC 843
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
763 GAGAGCGGTGGCGCTGCGCGCGCGGACAGCGCGCGAGCGCGGCAACGCGCAGACGTAC 822
QY 844 AATTCCAAATTTGATCAACATGTGGTTCAGGGGAGCGCGAGAGCGCGAGGCGCGATTGAG 903
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
823 AACAGAACCTGTATCAACAGTGGGAGAGGAGCGCGCAGAGAGCGCGGAGCATCGAG 882
QY 904 ACCTACATATTTGCGATTTCAACAGGATCAGAGAGCGCGCAGAGGATGAGAAATAC 963
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
883 ACCTACATTTTGGCATGTTCAACAGAAACAGAGAGGAGGAGCGAGAGAGGAGGAC 942
QY 964 TTTGGCTGTTTACCTTAAAGAGAGCGCTGTTTATTCATCAGCTTC 1011
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
943 TTGCGCTCTTCAACCCGAGCAGCTGCGCGCGCATACTCCATCAATTC 990

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RESULT 3

AAZ50051

ID AAZ50051 standard; cDNA; 1261 BP.

XX

```

AC AAZ50051;
XX 15-SEP-2003 (revised)
DT 04-MAY-2000 (first entry)
DT XX Mesocarp specific clone C23.
DE XX Clone C23; oil palm; regulatory sequence; beta glucanase activity;
KW tissue specific expression; mesocarp specific expression; fat; fatty oil;
KW 1,3 beta glucanase gene; ss.
XX Elaeis guineensis; Jacq.
XX FH Key Location/Qualifiers
FT CDS 28..1047
FT /*tag= a
FT /product= "Clone C23 protein"
FT /note= "Protein with beta glucanase activity"
XX PN WO200001804-A2.
XX PD 13-JAN-2000.
XX PF 14-JUN-1999; 99WO-EP004110.
XX PR 03-JUL-1998; 98EP-00305338.
XX PA (UNIL ) UNILEVER NV.
XX PA (UNIL ) UNILEVER PLC.
XX PI Kemp R, Stratford R;
XX DR WPI; 2000-182109/16.
XX DR P-PSDB; AAY44736.
XX PT DNA sequence useful for isolating regulatory sequences for tissue
XX PT specific expression of proteins in monocots especially oil palm plant.
XX PS Claim 2; Fig 3; 67pp; English.
XX CC The patent discloses a method for isolating regulatory sequences using a
XX CC beta glucanase gene. The regulatory sequence is used for tissue specific
XX CC expression of endogenous and exogenous proteins obtained from monocot
XX CC plants having drupaceous fruit. This promotes mesocarp specific
XX CC expression thereby, increasing the amount of fat or altering the relative
XX CC proportion of fatty acid in oil. Plants transformed with recombinant
XX CC vectors comprising the regulatory sequence are used in food or
XX CC pharmaceutical products. The present cDNA sequence is mesocarp specific
XX CC clone C23. Gene specific probes derived from the C23 are used to isolate
XX CC regulatory sequences from the mesocarp specific 1, 3 beta glucanase gene.
XX CC (Updated on 15-SEP-2003 to standardise OS field)
SQ Sequence 1261 BP; 393 A; 262 C; 250 G; 356 T; 0 U; 0 Other;

Query Match 38.2%; Score 430; DB 3; Length 1261;
Best Local Similarity 65.7%; Pred. No. 1.1e-99;
Matches 692; Conservative 0; Mismatches 350; Indels 12; Gaps 4;

QY 1 TTTATGGCAGCTCAGCAGCATCATCTCCATGGCTGCGCATGGCATCCCTCTGTAGTACTC 60
Db 25 TCCATGGCAACACCGAAGCAAGTATCCAGGGCTGCGGTGCGTACTTCAATGGACTCCTC 84
QY 61 TCGGCAATCCCGAGAGGGGTGGAATCCATTTGGGTCTGCAATGGATGAGCGGTGACAA 120
Db 85 GTAGCAATCCCAACAGGGGTGAAATCCATTTGGTGTGTATGGAATGAATGGAAACAAT 144
QY 121 CTCCCGCAGCGCGCGAGCTCGTCAACCTCTTCAAGTCCAAACATAGCTGGCATGCGA 180
Db 145 CTGCGCGAACCAGTGTGTGTGTAACCTCTATAAATCTAAATATCAACGCAATGAGG 204
QY 181 CTCTACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAATCTTACTCATC 240
Db 205 CTTTATGATCCAAACCAAGCTGCTCTCCAGGCCCTCCAGGGCTTCCAAACATCCAACTCATC 264

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Qy	241	CTGAGCGTCCCAAACTCGGACCTCCAAAA	CATTGCGCTCCGACCAATCGCGCGCACCAAC	300
Db	265	TTGGATGTCCAAATACTCGTCTCCAATCA	TATGGCTTCTAGCCCTTCAGCAGCTAAACAAT	324
Qy	301	TGGGTCCAAACCAACGTCCTCAAGCCTA	--CCCAAACGTTCGCTTCGATATCATCCGCGTC	357
Db	325	TGGGTCCAGCAAAATGTGAAGCCCTAT	CTCTCTGCTGTTTCATTTAAATATCATCGCAGTT	384
Qy	358	GGAAACGAAGTCAATCCCGCGGCGCAAG	TCAGTACGTCTCCAGGCATGAACAACAATA	417
Db	385	GGAAATGAAGTGATTCCTGGAGCTGAAG	CCCAATATGTGTCTCCGTCATGAGAAAATC	444
Qy	418	CAGTCGCGCCTCTCCTCTGCGGGCTT	CAGAAC--ATCAAGTCTCCACATCAGTCTCC	474
Db	445	TATTCAGCTCTTCTCTCGCTGGCTTACA	AAACCAATTAAGTCTCACTGCGAGTCGCC	504
Qy	475	TTGCGCGTCTCGGTACCTCATATPCC	CCCCCTCAGCTGGCTCTTCTTCGATGCATCG	534
Db	505	ACTTCAGTCTTGGGAAATCATTTCTCT	CCCTCACAAGGGGCAATCTCTTCTGCTGCAATG	564
Qy	535	TGCACATTTGGTCCAATCATACAGTTT	CTAGCCAGCAATGGCTCCCACTACTTGCACAAC	594
Db	565	ACATATTGAGTCCAAATAGTTTCAAT	TTTTGGCTAGTAATGAGCACCACCTCTGGTAAAT	624
Qy	595	ATCTACCCCTACTTTGAGCTATGCTGG	CAACTCCGGATCCATCGACCTCTCATAGCCCTC	654
Db	625	GTATACCCCTACTTCAGTTATGTGAAT	AAACCCGAAACCAATCAACATTTGAATATGCCTTG	684
Qy	655	TTTACTGCATCTGTACAGTCTGTACAG	ACGCGTCTACGTTTACAACAACCTCTTCGAT	714
Db	685	TTTACTTCCCGGGGATCTGATGACAG	ATGGAACAATATAAATATCAGAACCTCTTTGAT	744
Qy	715	GCCATGCTGCAACGCAATTTGACTCT	CGGCGCTTGAGAGCGCCGAGGCGCGAATGTCCCTGTT	774
Db	745	GCCATAGTTGATGCAATTTATGCGCA	TTGGAGAAGCTCGAGGGTCTAATGTGGCGATA	804
Qy	775	GTCTGTTCGGAGATGGCTGCGCGT	CTACGCGGCGGACAGCGGCGACGGTGTCTAATGCG	834
Db	805	GTGGTGTTCAGAGACGGTTGCGCCAT	CAGCTGGTGGTACTCGCAGCAACCATCAACAAATGCA	864
Qy	835	CAGACTTACAATTCCAATTTTGATCAA	CCATGTGGGTCAAGGACCGCGAAGAGGCCAGG-	893
Db	865	AAGACATATAATCAGAAATTTGATCA	ATCATGTTGTTCAAGGGACTCCAAGGAGATCTGGA	924
Qy	894	--GGCGAATTGAGACCTACATATTTG	CCCATGTTTCAACGAGGATCAGAGCAGCGCCAAAGG	951
Db	925	AAGGCTATAGAGGCTTACATATTCGA	ATTTGAGATGTTTCAATGAGAAATTTGAAATCATCG--	981
Qy	952	ATTGAGAAATACTTTGGGCTGTTTTT	ACCTTAAACGAACGCTGTCTATTTCGATCAGCTTC	1011
Db	982	ATTGAAACAAACTTTGAACTGTTTT	TCCCAATAATGCAACAGTCTACCCATCACTTT	1041
Qy	1012	ACTTGAGAAATTTGATCAGATGAAAT	ATAAATAA 1045	
Db	1042	ACTTGAATGCCAGGCGCATATAATAA	TAGTAA 1075	

RESULT 4

RESULT 4
ADT19801
ID ADT19801 standard; cDNA: 1439 BP.

AC ADT19801:

13-JAN-2005 (first entry)

XX DE Plant cDNA. Seq ID 5127.

XX Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomannan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;

seed protein yield.

viridiplantae.

US2004216190-A1.

28-OCT-2004

18-DEC-2003: 2003US-00739930

28-APR-2003. 2003US-00124E99

28-APR-2003; 2003US-00425115.

(KOVA/) KOVALIC D K.

Kovalic DK;

WPI; 2004-757369/74.

New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improved biological characteristics.

Claim 1: SEQ ID NO 5127: 14pp: English:

The invention relates a recombinant DNA construct comprising a polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant heat tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant tolerance to pathogens or pests, for yield improvement by modification of photosynthesis, for modifying seed oil yield and/or content, for modifying seed protein yield and/or content, for yield improvement by modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and development under at least one stress condition. The polynucleotide may also encode a plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and genetics, in particular for producing transgenic plants with improved biological characteristics such as increased yield, improved nitrogen flow, increasing plant tolerance to cold or heat, improving plant tolerance to extreme osmotic and drought conditions, and improving plant tolerance to plant pests or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and analysis systems. The present sequence is one of the 5544 plant cDNA sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20040216190.

Sequence 1439 BP: 308 A; 472 C; 398 G; 259 T; 0 U; 2 Other;

every Match 38.0%; Score 427.2; DB 13; Length 1439;

```

every Match      38.0%; SCORE 427.2; DB
1st Local Similarity 66.0%; Pred. No. 5.9e-99;

```

Seq. ID	Seq. Name	Seq. Length	Seq. Type	Seq. Source	Seq. Accession	Seq. Date	Seq. Status	Seq. Notes
1	Seq1	100	Protein	Human	NP_001234	2023-10-27	Active	Initial sequence
2	Seq2	100	Protein	Human	NP_001235	2023-10-27	Active	Initial sequence
3	Seq3	100	Protein	Human	NP_001236	2023-10-27	Active	Initial sequence
4	Seq4	100	Protein	Human	NP_001237	2023-10-27	Active	Initial sequence
5	Seq5	100	Protein	Human	NP_001238	2023-10-27	Active	Initial sequence
6	Seq6	100	Protein	Human	NP_001239	2023-10-27	Active	Initial sequence
7	Seq7	100	Protein	Human	NP_001240	2023-10-27	Active	Initial sequence
8	Seq8	100	Protein	Human	NP_001241	2023-10-27	Active	Initial sequence
9	Seq9	100	Protein	Human	NP_001242	2023-10-27	Active	Initial sequence
10	Seq10	100	Protein	Human	NP_001243	2023-10-27	Active	Initial sequence
11	Seq11	100	Protein	Human	NP_001244	2023-10-27	Active	Initial sequence
12	Seq12	100	Protein	Human	NP_001245	2023-10-27	Active	Initial sequence
13	Seq13	100	Protein	Human	NP_001246	2023-10-27	Active	Initial sequence
14	Seq14	100	Protein	Human	NP_001247	2023-10-27	Active	Initial sequence
15	Seq15	100	Protein	Human	NP_001248	2023-10-27	Active	Initial sequence
16	Seq16	100	Protein	Human	NP_001249	2023-10-27	Active	Initial sequence
17	Seq17	100	Protein	Human	NP_001250	2023-10-27	Active	Initial sequence
18	Seq18	100	Protein	Human	NP_001251	2023-10-27	Active	Initial sequence
19	Seq19	100	Protein	Human	NP_001252	2023-10-27	Active	Initial sequence
20	Seq20	100	Protein	Human	NP_001253	2023-10-27	Active	Initial sequence
21	Seq21	100	Protein	Human	NP_001254	2023-10-27	Active	Initial sequence
22	Seq22	100	Protein	Human	NP_001255	2023-10-27	Active	Initial sequence
23	Seq23	100	Protein	Human	NP_001256	2023-10-27	Active	Initial sequence
24	Seq24	100	Protein	Human	NP_001257	2023-10-27	Active	Initial sequence
25	Seq25	100	Protein	Human	NP_001258	2023-10-27	Active	Initial sequence
26	Seq26	100	Protein	Human	NP_001259	2023-10-27	Active	Initial sequence
27	Seq27	100	Protein	Human	NP_001260	2023-10-27	Active	Initial sequence
28	Seq28	100	Protein	Human	NP_001261	2023-10-27	Active	Initial sequence
29	Seq29	100	Protein	Human	NP_001262	2023-10-27	Active	Initial sequence
30	Seq30	100	Protein	Human	NP_001263	2023-10-27	Active	Initial sequence
31	Seq31	100	Protein	Human	NP_001264	2023-10-27	Active	Initial sequence
32	Seq32	100	Protein	Human	NP_001265	2023-10-27	Active	Initial sequence
33	Seq33	100	Protein	Human	NP_001266	2023-10-27	Active	Initial sequence
34	Seq34	100	Protein	Human	NP_001267	2023-10-27	Active	Initial sequence
35	Seq35	100	Protein	Human	NP_001268	2023-10-27	Active	Initial sequence
36	Seq36	100	Protein	Human	NP_001269	2023-10-27	Active	Initial sequence
37	Seq37	100	Protein	Human	NP_001270	2023-10-27	Active	Initial sequence
38	Seq38	100	Protein	Human	NP_001271	2023-10-27	Active	Initial sequence
39	Seq39	100	Protein	Human	NP_001272	2023-10-27	Active	Initial sequence
40	Seq40	100	Protein	Human	NP_001273	2023-10-27	Active	Initial sequence
41	Seq41	100	Protein	Human	NP_001274	2023-10-27	Active	Initial sequence
42	Seq42	100	Protein	Human	NP_001275	2023-10-27	Active	Initial sequence
43	Seq43	100	Protein	Human	NP_001276	2023-10-27	Active	Initial sequence
44								

21 CATCTCCATGGCTGCCATGGCATCCCTCCTTGTAGTACTCTCGGCAATCCCGAGAGGCGT 80

96 CATGTTTTCGGTGGCGTTGGCCCTTCTTGGAGTGCCTCTGGGATCCATTCTGCAGCGGT 155

Db 1262 GCGCGGGCTCGGGAACATCAAGGTGTCAGCTCGGTGTCACGCGGAGGTTCGCAAC 1321
 QY 493 TCATATCCCCCTCAGCTGGCTCTTCTCTCCGATGTCATCTCGACATTTGGTCCCAATC 552
 Db 1322 GGTTCGCGCGCTCGCGGGAGCTTCTCGGC-----TCGACATTTGGGGCCATA 1372
 QY 553 ATACAGTTTCTAGCAGCAATGGCTCCCATTTACTTTCGCAACATCTACCCCTACTTGGAC 612
 Db 1373 GGTCAGTACTCGGGAGCACCGGGGGCGCTGCTCGCCAACTCTACCCCTACTTTCGCC 1432
 QY 613 TATGCTGGCAATTCGGATTCATGACCTCTCATAGCCCTCTTACTGTCATCTGGTACA 672
 Db 1433 TACGTGGCAACAGGGGCCAGATGACATCAACTAGCGCTCTTACCGTTCGCGGGCAG 1492
 QY 673 GTCTGACAGAGCGGTCTTACGCTTTACCAACCTCTTCGATGCGCATGTCGACGCAATTG 732
 Db 1493 GTGTGTCAGGACGGCGGACCGTACCGAACCTGTTTCGACGCCATCTGTCGACAGTTTC 1552
 QY 733 TACTCGGCGCTGGAGAGCGCGGAGCGCGAATGTCTTGTGTCGTCGAGAGTGGC 792
 Db 1553 TACTCGGCGCTGGAGAGCGCGGAGCGCTCCGATGCTGTGTCGAGAGCGGG 1612
 QY 793 TGGCGCTCAGCGGGCGGACAGCGCGGAGCGGTCTTAATGCGCAGCTTCAATTTCCAAT 852
 Db 1613 TGGCGCTCAGCGGGCGGACAGCGCGGAGCGGTCTTAATGCGCAGCTTCAATTTCCAAT 1672
 QY 853 TTGATCAACCATGTGGTTCAGGGAGCGCGGAGAGCGCGGAGCGGTTCGACCTTACATA 912
 Db 1673 CTGATCAACCATGTGGTTCAGGGAGCGCGGAGAGCGGTTCGACCTTACATA 1732
 QY 913 TTTGCCATGTTCAACAGAGATCAGAGAGCGCGGAGAGCGGTTCGACCTTACATA 972
 Db 1733 TTTGCCATGTTCAACAGAGATCAGAGAGCGCGGAGAGCGGTTCGACCTTACATA 1792
 QY 973 TTTTACCTTACGAAACAGCTGCTTATTCGATCAGCTTC 1011
 Db 1793 TTTTACCTTACGAAACAGCTGCTTATTCGATCAGCTTC 1831

RESULT 7
 AAX25612
 ID AAX25612 standard; DNA; 3559 BP.
 AC AAX25612;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Banana ripening fruit Gluc. DNA.
 XX
 KW Banana; fruit ripening; glucanase; differential expression;
 KW fruit development; transgenic plant; ss.
 XX
 OS Musa acuminata.
 XX
 PN WO9915668-A2.
 XX
 PD 01-APR-1999.
 XX
 PP 23-SEP-1998; 98WO-US003343.
 XX
 PR 25-SEP-1997; 97US-0060062P.
 XX
 XX (BOYC-) BOYCE THOMPSON INST PLANT RES.
 XX
 PI May G, Clendennen S;
 XX
 DR WPI; 1999-244425/20.
 DR P-PSDB; AAY05839, AAY05840, AAY05841.
 XX
 PT New isolated banana DNA molecules.
 XX
 PS Disclosure; Fig 15A-E; 143pp; English.

XX This is the nucleotide sequence of a DNA molecule termed GLUC. The
 CC invention provides isolated DNA molecules which are differentially
 CC expressed during banana fruit development, and the protein products of
 CC these genes. The DNA is selected from a group comprising starch synthase,
 CC chitinase, endochitinase, beta-1,3-glucanase, thaumatin-like protein,
 CC ascorbate peroxidase, metallothionein, lectin and senescence-related
 CC protein. The regulatory elements of the genes can be used to produce
 CC chimeric genes for transformation of plants to provide controlled
 CC expression of heterologous DNA during fruit development, or in response
 CC to exogenous developmental signals, such as ethylene signals. The
 CC heterologous protein, e.g. a therapeutic protein, can be isolated from
 CC the fruit or consumed directly in the transformed fruit. The identity of
 CC the present sequence is not given. The entire DNA sequence has been
 CC decoded in all 3 reading frames to provide the amino acid sequences given
 CC in AAY05839-41
 SQ Sequence 3559 BP; 1008 A; 776 C; 725 G; 1050 T; 0 U; 0 Other;
 Query Match 36.9%; Score 415.6; DB 2; Length 3559;
 Best Local Similarity 68.2%; Pred. No. 7,7e-96;
 Matches 570; Conservative 0; Mismatches 294; Indels 18; Gaps 6;
 QY 75 AGGCGTGGAAATCCATTTGGGTCTGCAATGGAATGGAACGATGCGATGCGACCTTCCCGCCCGC 134
 Db 2078 AGGAGTGCATATCGATTTGGTGTCTGCTACGGAATGCTCGGCAACAATCTTCCCGCCCGC 2137
 QY 135 CGAGTGTGCTCAACTCTCAAGTTCACAAACATAGTGGCATGCGACTCTACAGCCCGCA 194
 Db 2138 CGAGTGTGCTCAACTCTCTACAAATCCAAACATCGGAGGATGAGACTCTACGATCCAAA 2197
 QY 195 CCAAGCCACTCTCCAGGCCCTCCAGGGCTTAAACATCTACCTCTCTCTCGAGTCCCGCAA 254
 Db 2198 CCAGCGCCCTCGAGCCCTCAGAACTCCAAATCCAAATCTGTTGGATGTTCCCGCG 2257
 QY 255 CTCGAGCTCCAAACATTTGCTCCGACCAATCCGCGCCGACCACTCGGTTCCAAACCAA 314
 Db 2258 ATCCGAGTGCAGTCACTGGCTCCAAATCTTTCGCGCGCGGAGTCCGAGGAA 2317
 QY 315 GGTCCAGCTTAC---CCAAACGTTGCTTCGATACATACGCGTCCGAAACGAGTCAAT 371
 Db 2318 GGTGCTGCTTACTTGGCCCGAGCTCTCTCTTTCGATACATAGCTGTGCGGAAACGAGCTGAT 2377
 QY 372 CCCCG---CGGCCAAGCTCAGTACGCTCTCCAGCCATGAACATACATACAGTCCGCCCT 428
 Db 2378 CCCCGATCGATCTGGCGAGTACATCTCTCCCGCATGCGCAACATCTCAATGCTTT 2437
 QY 429 CTCTCTGCGCGCTTCAGAAC---ATCAAGGTCTCCACATCAGTCTCTTTCGGCGTCT 485
 Db 2438 GTCTCTGCGCTGCTGCAAAACAGATCAAGTCTCGACCGCGGTTCGACACGGGGCTCT 2497
 QY 486 CGGTACCTCATATCCCGCTCAGTGGCTCTTCTCTTCGATGATGATGATGATGATGATGAT 545
 Db 2498 CGGCACGTCTTACCTCTCCCGCGCGCTTCTCTCTCCCGCGCGGAGGAGTACCTGAG 2557
 QY 546 TCCATCATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTCCCAATCTACCCCTA 605
 Db 2558 CCCCATGTGCGATCTTGGCGAGTACGAGCGCGCTCTCTGTTCAATGTGATCCCTTA 2617
 QY 606 CTTGAGCTTATGCTGGCAACTCTCGGATCCATCGACTCTCTCATACGCCCTCTTTCATGCAATC 665
 Db 2618 TTTTAGCTACACCGGCAACCGGGACAGATCTCGCTGCTCTACGCCCTGTTCCGCGCTC 2677
 QY 666 TGGTACAGTCTGACAGAGCGTCTTAGGCTTACAAACCTCTTTCGATGATGATGATGATGAT 725
 Db 2678 CGGCCTGCTGCTGAGGATGAGGAGTTCAGCTATCAGAACTGTTTCGACGCGCATCTGCA 2737
 QY 726 CGCATTTGCTTCTCGGCCCTTGGAGAGCGCGGAGGCGCGAATGCTCTGTTGCTGTCGGA 785
 Db 2738 CGCGGTCTTTCGCGCGCTTGGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2797
 QY 786 GAGTGGCTGCGCGTTCAGCGCGCGGAGCAGC---GGCGAGCGGTGCTTAATGCGCAGACTTA 842

QY 988 CAGCGTGTCTATTCGATCAGCTTC 1011
 Db 889 TCGCGGCATACCTCCATCAATTC 912

RESULT 9

AAQ24291
 ID AAQ24291 standard; DNA; 1463 BP.

AC AAQ24291;

XX 02-NOV-1992 (first entry)

XX (1-3,1-4)-beta-glucanase isoenzyme EI (2).

XX Distal promoter; EI; beta-glucan; endosperm; beer production; ss.

XX Hordeum vulgare.

XX Key Location/Qualifiers
 CDS 68..1072

FT /*tag= a

FT /label= EI

FT 68..151

FT /*tag= b

FT sig_peptide

FT 152..1069

FT /*tag= c

FT mat_peptide

FT 1410..1414

FT /*tag= d

FT polyA_signal

FT 1410..1414

FT /*tag= d

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FT 1410..1414

FT /*tag= d

PS Disclosure; Fig 9; 75pp; English.
 XX This sequence encodes the 1463bp cDNA of barley (1-3,1-4)-beta-glucanase isoenzyme EI. This sequence is derived from a transcript from the distal promoter of the (1-3,1-4)-beta-glucanase isoenzyme EI gene. (See also AAQ24290.) EI is synthesized in germinating barley grain where it acts to depolymerise the beta-glucans in the cell walls of the starch endosperm. Low levels of the enzyme leads to high levels of the glucans and this can cause a reduced malt quality, serious filtration difficulties in the brewing process and can contribute to haze formation in the final product. The isolated EI gene can be transferred to plants to generate varieties which have improved malting and brewing properties.
 CC Alternatively the gene can be introduced into yeast to remove residual beta-glucan in beer prodn. This protein can be mutated to generate a more thermostable enzyme

XX Sequence 1463 BP; 303 A; 468 C; 421 G; 271 T; 0 U; 0 Other;

Query Match 36.3%; Score 408.6; DB 2; Length 1463;

Best Local Similarity 64.0%; Pred. No. 3.5e-94;

Matches 650; Conservative 0; Mismatches 359; Indels 6; Gaps 2;

QY 4 ATGGAGCTCAGCAGCATCATCTCCATGGCTGCGATCCCTCTGTAGTACTTCG 63

Db 68 ATGGAGGCCAAGGGTTGGCTCCATGTTGGCTCTGGCATGCTCTCGAGCCTTCGCC 127

QY 64 GCAATCCGAGAGGCGTGGAAATCCATTTGGGGTCTCAATGGAATGAGCGGTGACAACTTC 123
 Db 128 TCCATCCCAACAAGCGTGGAGTCCATCGGGTGTCTAGCGCATGAGCGCAACATCTG 187
 QY 124 CCCAGCGCGCGAGCGTCTCAACTCTTACAGTCCAAACAATAGTGGGATGAGCTC 183
 Db 188 CCGCGCGGAGCACCCTGTGTTCAAGTCTCAAGTCCAAACGGGATCAACTCCATCGGGTG 247
 QY 184 TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTC 243
 Db 248 TAGCTCTCCGACAGCGCGGTGAGGGGTGCGGCGCAACGGGCTGAACTGTTGTG 307
 QY 244 GAGTCCCAACTCCGACCTCCAAACAATTGCTCCGACCAATCCGCGCCCAACCAACTGG 303
 Db 308 GCGCGCCCAACGACGTCTCTCCAACTCCGCGCAGTCCCGCAGCGCTCATCGTGG 367
 QY 304 GTCCAAACAAGTCCCAAGCTTACCCAAAGCTTGGCTTCGATATCATCGCGTCCGAAAC 363
 Db 368 GTGAGGAGCAATCATCCAGCGGTACCCCAAGTCTCTCCGATAGTCTGCGTGGGCAAC 427
 QY 364 GAAGTCATCCCGCGCGCAAGCTCAGTACGTCTCCAGCCCATGAAACAATACAGTCC 423
 Db 428 GAGG---TCCCCGGCGCGCCACCCAGAACCTTGTCCCCCGCATGAGAACGTGCGGGC 484
 QY 424 GCCCTCTCTGCGCGCTTTCAGAACATCAAGGTCTCCACATCAGTCTCTCTTCGGCGTC 483
 Db 485 GCGTGGCTCTCGCGCGGTGGGCCACATCAAGGTGACCACTGCGTCTCGCAGGCCATC 544
 QY 484 GTCGGTACTCATATCCCCCTCAGTGGCTCTCTCTTCGATGATCATGTCGATG 543
 Db 545 CTGGGGGTGTACAGCCCGCGCTCCGCGGTCTTACCGGAGAGCGGCGTTCATG 604
 QY 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCACTTACTTGGCAACATCTACCCC 603
 Db 605 GGGCCCGTGGTGCAGTCTCTTGGCGCACCCGCGCGCTCATGGCCAAACATCTACCCG 664
 QY 604 TACTTGAGCTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCGCTCTTTACTGCA 663
 Db 665 TACCTGGCTGGGCTTACACCCGCGCATGACATGAGCTAGCGCTCTTACCGCC 724
 QY 664 TCTGTACAGTCTGACAGGCGGTCTTACCTTACAAACACTCTTCGATGCCATGTC 723
 Db 725 TCCGCAACCGTGTCTCAGGACGGTCTCTTACGGGTACCAAGAACCTGTTCCGACACCCG 784
 QY 724 GACCATTTGTTACTCGGCCCTGAGAGCGCCGAGGGCGCAATGTCCTGTTGTGCTGTCG 783
 Db 785 GACGCTTTTACACGCGCCATNGGCCAAGCACGCGCGCTCCAAACGTGAAGCTGGTGTGTC 844
 QY 784 GAGAGTGGCTGGCGCTCAGCGGGGAGACGCGGCTGTCTAATGCGCAGACTTAC 843
 Db 845 GAGAGCGGTGGCGCTCAGCGCGGCGACGCGCGGCGACCCCGCCACGCGCAGGATCTAC 904
 QY 844 AATTCCAAATTTGATCAACCACTGTTGGGTGAGGGGACGCGGAGAGAGGCCAGGGCGATGAG 903
 Db 905 AACCAGTACCTCATCAACCACTGTTGGGTGAGGGGACCCCGCCCGCGCGCATCGAG 964
 QY 904 ACCTACATATTTGCTATGTTCAACGAGATCAGAGCGCGCGCAGGATTTGAGATTAAC 963
 Db 965 ACCTACGCTTTCTCTCATGTTTCAACGAGAACCAAGGA---CAACGGCGTGGAGCAGAAC 1021
 QY 964 TTTGGGCTGTTTACCCTTACGACAGCTCTCTTATGATCAGCTTCACTTGG 1018
 Db 1022 TGGGGGCTCTTCTTACCCCAACATGACGACGCTCTACCCCATCTGATGAG 1076

RESULT 10

ADT19681

ID ADT19681 standard; cDNA; 1458 BP.

XX ADT19681;

DT 13-JAN-2005 (first entry)

XX Plant cDNA, Seq ID 5007.
XX Plant; ss; gene; transgenic; cold tolerance; growth rate;
XX drought tolerance; disease resistance; galactomannan production;
XX plant growth regulator; heat tolerance; herbicide tolerance;
XX lignin production; extreme osmotic condition tolerance;
XX pathogenesis resistance; pest resistance; yield improvement; seed oil yield;
XX seed protein yield.
XX Viridiplantae.
OS US2004216190-A1.
XX 28-OCT-2004.
XX 18-DEC-2003; 2003US-00739930.
XX 28-APR-2003; 2003US-00424599.
PR 28-APR-2003; 2003US-00425115.
XX (KOVA/) KOVALIC D K.
XX Kovalic DK;
XX WPI; 2004-757369/74.
XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.
XX Claim 1; SEQ ID NO 5007; 14pp; English.
XX The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed a
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved nitrogen
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant cDNA
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 1458 bp; 310 A; 436 C; 417 G; 295 T; 0 U; 0 Other;

Query Match		35.0%	Score 394.2;	DB 13;	Length 1458;
Best Local Similarity		64.9%	Pred No. 1.7e-90;		
Matches 617; Conservative 0;		Mismatches 328;	Indels 6;	Gaps 2;	
QY	75	AGGCGTGGAAATCCATTTGGGGTCTGCAATGGAAATGACGATGACCAACCTCCCGGAGCCGCG	134		
Db	108	AGGCGTGGAGTCCATCGGGGTGTGCTACGGCATGAGCGCCCAACCACTGCCGGCGGCGAG	167		
QY	135	CGAGCGTGTCAACTCTCAAGTCCAAACATAGTGGCATGACGACTCTACAGCCCCGA	194		
Db	168	CACCGTGTGAGCATGTTCAAGTCCAAACGATCAACTCCATGCGGCTATATGCCCCCGA	227		
QY	195	CAAAGCCACTCTCCAGGCGCTCCAGGCGCTTAAACATCTACCTCATCTCCGAGTCCCGCAA	254		
Db	228	CAAGCGGCGCTGACAGGCCGTTGGGGGTACGGGCGTCAACGCTGCTGTCGGGGCGCCTAA	287		
QY	255	CTCCGACCTCCAAACATTTGCTCCGACCAATTCGCGCGCCCACTGGGTCCAAACCAA	314		
Db	288	CGAGTGTCTCTCCAAACCTCGCGCGCGCGCGCGCGCTCGTGGGTGAGGAGCAA	347		
QY	315	CGTCAAGCCTACCCAAACGTTGCTTCCGATACATCGCCGTCGGAAACGAGATCATCC	374		
Db	348	CATCCAGGCTACCCGAGGTTTCTTTTCGGTACGTCGCTGCGTCCGCAACGAGG---TCGC	404		
QY	375	CGGCGGCCAAGCTCAGTACGTCCTCCAGGCCATGAACAAACATACAGTCCGCGCTCTCCTC	434		
Db	405	CGGCGGTGCCACCAAGAACCTCTGTCGCGCGCATGAAACACGTCGAGGCGCGCTCGCCTC	464		
QY	435	TGCGCGCCTTCAGAACATCAAGGTCTCCACATCAGTCTCTTTCGCGCGTCGTCGGTACCTC	494		
Db	465	CGCTGGGCTGGGCCACATCAAGGTCAACACGTCGTCGCGAGGCCATCTCTCGGGGTGTA	524		
QY	495	ATATCCCCCTCAGTGGCTCTCTCTTTCGATGATGATGTCGATGTCGATGTCGATGTCGAT	554		
Db	525	CAGCCCGCCTTCGCGCGGCTCTTTCACGGGGAGCGGAGCGGTCATCGGGCGCGCTGGT	584		
QY	555	ACAGTTTCTAGCAGCAATGCTCCCAATTACTTTCGCAACATCTACCCCTACTTGGAGTGA	614		
Db	585	GCAGTTCCTTCCCGCACCGCGCGCGCTCATGGCCAAACATCTACCCGTCCTGCGCTG	644		
QY	615	TGCTGGCAATCTCCGATGTCATCGACCTCTCATAGCCCTCTTTACTGTCATCTGGTACAGT	674		
Db	645	GGCTTACAAACCGAGCGCATGAGCATGAGTACGGGCTCTTTCACCGGTCGCGCACCGT	704		
QY	675	GCTACAGACGGGTCTTACGCTTACAAACACTCTTCGATGCGCATGTCGAGCATTTGTA	734		
Db	705	GCTCAGGACGGCTCTTACGGGTACCAAGACCTGTTTCGACACCAACCGCTGGACGCTTCTA	764		
QY	735	CTCGGCTGAGAGCGCGGAGCGCGAATGTCCTCTGTCGTCGCGAGGTGGCTG	794		
Db	765	CACGGCCATGCCAAGCACCGCGCGCTCCACGTAAGCTCGTGGTTCGAGAGCGGGTG	824		
QY	795	GCGCTCAGCGCGGGGACAGCGCGGAGCGGTGTCTAATGCGCAGACTTACAAATTCCAATTT	854		
Db	825	GCCCTCAGCGCGGCGACGCGGCGGAGCTCCCGGCCAACCGCCGGATCTACACCACTACT	884		
QY	855	GATCAACCATGTTGGGTCAAGGAGCGCCGAGAGCGCGAGGGCGGATTTGAGACCTACATATT	914		
Db	885	CATCAACCATGTCGGGCGCGCACCCCCCGCCACCCCGGCGCCATCGAGAGCTTACGCTTT	944		
QY	915	TGCCATGTTTCAACGAGGATCAGAGCAGCGCGGATTTGAGATATACCTTTGGGCTGTT	974		
Db	945	CTCCATGTTTCAACGAGAACCCAGAGGA---CAGCGGGGTGGAGCAGAACTGGGGACTCTT	1001		
QY	975	TTACCTTAACGAACAGCGCTGTCTTTCGATCAGCTTCTACTTGGAGAAATTTG	1025		
Db	1002	CTACCCCAACATGACGACAGCTCTACCCCATCAGCTTCTGATGAGCTAGCTG	1052		

RESULT 11
AAQ24292
ID AAQ24292 standard; DNA; 1257 BP.
XX

XX Unidentified.
OS US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIU/J) LIU J.
XX PA (ZHOU/J) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABA/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX Claim 1; SEQ ID NO 26408; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 1268 BP; 276 A; 439 C; 336 G; 217 T; 0 U; 0 Other;
Query Match 33.9%; Score 381.6; DB 13; Length 1268;
Best Local Similarity 62.9%; Pred. No. 2.7e-87;
Matches 629; Conservative 0; Mismatches 359; Indels 12; Gaps 2;
QY 18 CATCATCTCCATGGTGGTGGCATGGCATCTCTTGTAGTACTCTCGGCAATCCCGAGAGG 77
DB 87 CGTGGCTTCCATGGATGGCTGGCATCTTCTCGGAGCATTCGAGCATCTCTACAGG 146
QY 78 CQTGGAATCCATTTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCGAGCGCCGA 137
DB 147 AGTCAATCCATCCAGCGGTGTGCTAGCGGTGAGCGGAGCAACTGCCCCCGGAGGCA 206
QY 138 CGTGTCAACCTCTTAAAGTCAACAACATAGCTGGCATGCGACTCTACAGCCCCGACCA 197
DB 207 CGTGGTGCAGCTGTACCATGTCACCGCATCAACCTGATGCGCATCTACTTCCCGAGCG 266
QY 198 AGCCTCTCCAGGCCCTCCAGGCTCTTAACTCTACCTATCTCTCGAGCTCCCACTC 257
DB 267 CAACCGCTGAAACCGCGCTGAGCGGACCCAGCATCGGGCTCATCTGAGAGTCCCAACAC 326
QY 258 CGACTCTCAAAACATTTGCTCTCGACCAATTCGCGCGCCCACTGGGTCCCAACCAAGT 317

DB 327 GGACTCGCCTCGCTGGCCTCCGACCCGAGCGCGCGCGCTCGGGTGAGAGCAAGT 386
QY 318 CCAAGCCTACCCAAACGTTTGGCTTCGGATACATCGCGTTCGAAACGAGTCAATCCCGG 377
DB 387 GCAGCGTTCCTCGCTGAGCTTCGCTACATCGCGTGGGCAACGAGG---CCTCCGG 443
QY 378 CGGCAAGCTCAGTACGTCCTCCAGCCATCAACAAATACATAGTCCGCGCTCTCTCTGCG 437
DB 444 CGGGACACCGGAGCATCTTCCCGCATGAGAACTCAACGCGGCGCTGGCCAGCG 503
QY 438 CGGCTTTCAGAAACATCAAGGTCTCCATCATAGTCTCTCTTCGGCGCTGCTGCGTACCTATA 497
DB 504 CGGCTGGCGGAGCATCAAGGTGTCCACGGCGGTGCAGAGCGAGGTCAACCGGGCTT 563
QY 498 TCCCGCTCAGCTGGCTCTCTTCTTCGATGCGATGCTGCGATTTGGGTCCAATACACA 557
DB 564 CCGCGCGTTCGAGGGCACCTTCTCGCAGGGCTACATGGCG-----CCCATCGCGCA 614
QY 558 GTTCTAGCCAGCAATGGCTCCCATTAAGTCTTGGCAACATCTACCCCTACTTTGAGCTATGC 617
DB 615 GTACTGAGAGCACCGGCGCGCTGCTGTGCAAGCTCTACCCCTACTTCTCTCAT 674
QY 618 TGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACTGTCATCTGGTACAGTCTG 677
DB 675 CGGCAACCGGCGCAGATCGACCTCAGCTACGCGCTCTTCACTCGCGGCGACCGTCTG 734
QY 678 ACAGGACGGTCTTACGCTTCAACAACCTTTCGATGCGCATGGTTCGAGCATTTGATCTC 737
DB 735 GCAGGACGGCAGCAACCGCTACAGAACTCTTCGACGCGCTCGTTCGACACCTTCTGCTC 794
QY 738 GGCCCTGGAGAGCGCGGAGCGCGAATGTCCTGTTGCTGTCGGAGAGTGGCTGGCC 797
DB 795 CGCGCTCAGAAACCGCGCGCGCGGCGGACGCTCCAGTGTCTGTCGGAGAGCGGTGGCC 854
QY 798 GTCTAGCGCGGAGCAGCGCGCGAGCGGTCTTAATGCGCAGACTTACAAATTCGAATTTGAT 857
DB 855 GTCCGCGGGGCGAGCGCGCGCACCGCGGCGCAACGCGCAGACCTACAAACCAAGAACCTCAT 914
QY 858 CAACATGTTGGTTCAGGGGAGCGCGAGAGCGCGAGCGCGGCGGATTTGAGACTTACATTTGCG 917
DB 915 CAACCATGTCGGCAGGGCAGCGCGCAAGCGCGCTGGCGCCCATCGAGACTTACATCTTGGC 974
QY 918 CATGTTCAACGAGATCAGAGCAGCGCGAGCGCGAGGATTTGAGAAATTAATTTGGCTGCTTTTA 977
DB 975 CATGTTCAACGAGACCAAGAGCAGCGGAGCGGAGTTCGAGAGGCACTTCGGCTCTTCAA 1034
QY 978 CCCTAAACGAGCAGCTGTCTATTGATCGATCAGCTTCACTTGA 1017
DB 1035 CCGGACAAATCGCGGCGGTACCCCATCAATTTCTCTCTAA 1074
RESULT 13
AAQ24290
ID AAQ24290 standard; DNA; 4643 BP.
XX AC AAQ24290;
XX DT 02-NOV-1992 (first entry)
XX DE (1-3,1-4)-beta-glucanase isoenzyme EI.
XX DE Distal promoter; proximal promoter; introns; signal peptides; EI;
KW beta-glucan; endospore; beer production; ss.
XX OS Hordeum vulgare.
XX FH Key Location/Qualifiers
FT TATA_signal 420..430
FT /tag= b
FT /note= "Distal promoter, see comments"
FT misc_signal 474
FT /tag= c
FT /label= Transcription_start_point

CDS /note= "Distal promoter"
546..4064
/*tag= a
/label= E1
546..3143
/*tag= e
/note= "Distal promoter, see comments"
619..3132
/*tag= d
/note= "Distal promoter, see comments"
836
/*tag= g
/label= Transcription_start_point
/note= "Proximal promoter"
2797..2807
/*tag= f
/note= "Proximal promoter, see comments"
3020..3143
/*tag= i
/note= "Proximal promoter, see comments"
3078..3132
/*tag= h
/note= "Proximal promoter, see comments"
3144..4061
/*tag= j
/label= E1
4399..4404
/*tag= k
/note= "Both promoters"

WO9205258-A.
02-APR-1992.
20-SEP-1990; 90AU-00002401.
20-SEP-1990; 90AU-00002401.
(UYLT-) LA TROBE UNIV.
Fincher G;
WPI; 1992-150484/18.
P-PSDB; AAR23601, AAR27060.
DNA encoding barley (1-3,1-4)-beta-glucanase isoenzyme(s) E1 and E11 -
used to improve quality of barley for malting and brewing processes.
Disclosure; Fig 1; 75pp; English.
This sequence encodes (1-3,1-4)-beta-glucanase isoenzyme E1 gene, showing
the two promoter regions, the distal and proximal promoters. The two
transcripts produce the same mature protein but have different signal
peptides. The transcript from the distal promoter is 4169bp long and
contains an intron of 2513bp. This intron is unusually long for a plant
intron which have an average length being 249bp. The signal peptide
produced from this transcript is 28 amino acids long. The transcript from
the distal promoter is 3807bp and contains an intron of 54bp. The signal
peptide produced from this transcript is 23 amino acids long. There is
some evidence that suggests that these differing introns may have some
role in exon "shuffling". E1 is synthesized in germinating barley grain
where it acts to depolymerise the beta-glucans in the cell walls of the
starchy endosperm. Low levels of the enzyme leads to high levels of the
glucans and this can cause a reduced malt quality, serious filtration
difficulties in the brewing process and can contribute to haze formation
in the final product. The isolated E1 gene can be transferred to plants to
generate varieties which have improved malting and brewing properties.
Alternatively the gene can be introduced into yeast to remove residual
beta-glucan in beer prodn. This protein can be mutated to generate a more
thermostable enzyme

Sequence 4643 BP; 1166 A; 1190 C; 1110 G; 1177 T; 0 U; 0 Other;

Query Match 33.8%; Score 380.8; DB 2; Length 4643;
Best Local Similarity 64.2%; Pred. No. 7e-87;
Matches 606; Conservative 0; Mismatches 332; Indels 6; Gaps 2;
QY 75 AGCGTGGGAATCATTTGGGGTCTGCAATGGAATGGAGCGGTGACAACTCCCCAGCGCCG 134
Db 3131 AGCGTGGAGTCCATCGGGGTGTGCTACGGCATAGCGCAACAATCTGCGCGCGGAG 3190
QY 135 CGACGTCGTCAACCTCTCAAGTCCAAACAACTAGCTGGCATCGCATCTCTACAGCCCCGA 194
Db 3191 CACCGTGGTCAACATGTTCAAGTCCAAACGGGATCAACTCCATGGCGGTGTACGCTCCGA 3250
QY 195 CCAAGCCACTCTCCAGGCGCTCCAGGGCTCTTAACATCTACCTCATCTCGAGCTCCCAA 254
Db 3251 CCAGGCGGCTGCGAGCGGTGCGGCGCACGGCGGTGAACGTTGTTGTGGCGCGCCAA 3310
QY 255 CTCGACCTCCAAACATTTGCTCCGACCAATCCGCGCGCAACAACCTGGGTCCAAACCA 314
Db 3311 CGACGTGCTCTCAACCTCGCGCGAGTCCCGAGCGGTGCATCGTGGGTGAGGAGCAA 3370
QY 315 CGTCAAGCTTACCCAAACGTTTGCCTTCCGATACATCGCGCTCGGAACGAAAGTCAATCC 374
Db 3371 CATCCAGGGTACCCCAAGTCTCTTCCGGTATGCTCTCGGTGGGCAACAGG---TCGC 3427
QY 375 CGCGCGCAAGCTCAGTACGTCTCCAGCCATGAACAAACATACAGTCCGCGCTCTCCTC 434
Db 3428 CGCGCGGCGCACCCAGAACCTTTGTCCCGCCATGAAGAGCGTGCAGGCGCGCTGGCCTC 3487
QY 435 TCGCGGCTTCAAGACATCAAGGTCTCCACATAGTCTCTCTTCGGGCGTGTGGTACCTC 494
Db 3488 CGCGCGGCTGGGCGCACATCAAGGTGACCAAGTGTGCGAGGCCATCTCGGGGTGTA 3547
QY 495 ATATCCCGCTCAGCTGGCTCTCTTCCGATGATCGCTCGACATCTGGGTCCCAATCAT 554
Db 3548 CAGCGCGCGCTCCGCGGCTCTTCCGAGAGGCGGAGCGGCTTCATGGGCGCGGTGGT 3607
QY 555 ACAGTTTCTAGCCAGCAATGGCTCCCGCATTTATTCGCAACATCTACCCCTACTTGAAGTA 614
Db 3608 GCAGTTCTTGGCGCGCACCGCGCGCTCATGCGCAACATCTACCCCTACTTGGCCTG 3667
QY 615 TGCTGGCAACTCCGGATCCATCGACTCTCTATACGCGCTCTTTATCGCATCTGGTACAGT 674
Db 3668 GGCCTTACAAACCGAGCGCATGGAACATGAGCTACGCGCTCTTACCGCTCCGCGCACCGT 3727
QY 675 CGTACAGACGCGTCTTACGCTTACAAACCTCTTCGATGCCATGGTTCGAGCGCATGTA 734
Db 3728 GGTCCAGACGCGCTCTTACGCGGTACCAAGAACCTGTTCCGACACCCGCTGGAGCGCTTCTA 3787
QY 735 CTCGCGCTTGGAGAGCGCGGAGGCGCAATGTCCTGTGTCGTGTCGAGAGTGGCTG 794
Db 3788 CACGCGCATGGCCAGACAGCGCGGCTCCACGTTGAAGTGGTGGTTCGAGAGCGGGTG 3847
QY 795 GCGGTCAGCGGCGGAGACAGCGGCGACCGGTGTCTTAATGCGCAGACTTACAATTTCCAAATTT 854
Db 3848 GCGGTCAGCGGCGGACAGCGGCGGACCCCGCGCAACCGCAGGACTCTACAACAGGTACCT 3907
QY 855 GATCAACCATGTGGTTCAGGGGAGCGCCGAGAGGCGGCGGCGATGAGACCTACATATT 914
Db 3908 CATCAACCATGTGGGCGCGGCGCACCCCGCGCACCCCGCGCGCATCGAGACCTAGCTCTT 3967
QY 915 TGCCATGTTCAACGAGGATCAGAACGCGCAGCGGATTCGAGATAACTTTGGGCGTGT 974
Db 3968 CTCATGTTCAACGAGAACCGAGAGGA---CAACGCGGTGGAGCAGAACTGGGGGCTCTT 4024
QY 975 TTACCTTAACGACAGCGCTGTCTATTTCGATCAGCTTCTCACTTTGAG 1018
Db 4025 CTACCCCAACATGACGACGCTTACCCCATCAGCTTCTGATGAG 4068

RESULT 14
ADL18243
ID ADL18243 standard; DNA; 4849 BP.
XX

XX Zhu T, Wang X, Chang H, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Moughamer T, Provart N, Ricke D;
XX WPI; 2003-829655/77.
XX P-PSDB; ADJ11804.
XX New polynucleotide, useful for modulating gene expression within a cell
PT by posttranscriptional gene silencing.
XX
XX Example 15; SEQ ID NO 439; 79pp; English.
XX This invention relates to a novel method for identifying isolated
CC polynucleotides that are modulated by post-transcriptional gene silencing
CC (PTGS). Specifically, it refers to the regulation of gene expression in
CC plants via PTGS and the trans-activation of homologous genes due to
CC increased RNA degradation. The present invention describes clusters of
CC polynucleotides from cereals, in particular rice, as well as homologues
CC and the polypeptide sequences derived thereof, where gene expression is
CC altered in response to PTGS. As such, the elucidation of gene silencing
CC mechanisms can lead to more efficiently expressed transgenes, and can
CC also improve the understanding of plant-viral interactions and targeting
CC the suppression of specific plant genes. This polynucleotide sequence is
CC a rice cDNA sequence where expression is modulated by gene silencing,
CC given in an exemplification of the invention. NOTE: This sequence does
CC not appear in the printed specification but has been obtained in
CC electronic format from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20030135888.
XX
XX Sequence 1110 BP; 197 A; 326 C; 402 G; 185 T; 0 U; 0 Other;

Query Match 31.5%; Score 354.2; DB 11; Length 1110;
Best Local Similarity 60.9%; Pred. No. 2.7e-80;
Matches 613; Conservative 0; Mismatches 388; Indels 6; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCG 63
DB 1029 ATGGCTAGCAAGGTGTAGCCCTCCATGTTTCGCTCTCGCATTCCTCTCGGTGCTTGGC 970
QY 64 GCAATCCCGAGAGGGTGGAAATCCATTGGGGTCTGCAATGGAATGGAGGTGACAACTTC 123
DB 969 TCCATCTCTCAAGAGGGAGGGGATCGGGGTGTGCTAGCGCATGAGCGCGAACAACCTG 910
QY 124 CCCCAGCCCGCGAGCTCGTCAACCTCTCAAGTCCAAACAACATAGCTGGCATGCGACTC 183
DB 909 CGCGCGGAGCTCGGTGTGGGGATGTACCGCTCCACGGCATCAGCTCGATCGGGCTG 850
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTCATCTCTC 243
DB 849 TACGCGCCGGACAGGCGGCGCTGCACTCGTGGGGCGGACCGGGGATCAGCGTCTGCTC 790
QY 244 GAGCTCCCAACTCCGACCTCCAAACAATTGCTCCGACCAATCCGCGCCACCAACTGG 303
DB 789 GCGCGGCCCAAGCATGTCTCTCAACCTTCGCGCGCAGCCCGCGCGCGCGCTCGTGG 730
QY 304 GTCCAAACCAAGCTCCAGCTTACCAAAAGCTTGGCTTCCGATACATCGCGCTCGGAAAC 363
DB 729 GTGCGGAACACATCAGGCTTACCGCTCGGTGTGTTCCGTAAGTCCGCTCGGGAAC 670
QY 364 GAAGTCATCCCGCGGCGGCAAGCTCAGTACGTCTCCAGGCCATGAAACAACATACAGTCC 423
DB 669 GAGG---TCGCGCGGCGGCGGACGTCAGCTCCAGCTGGTCCCGGCCATGGAGAACGTCCGCGGC 613
QY 424 GCTCTCTCTCTGCGGGCTTTCAGAAACATCAGGTCTCCACATAGTCTCTTTCGGGCTC 483
DB 612 GCGCTGGGTGTGCGCGGGGCTGGGCCACATCAAGGTGACGACGTCTGCTGTCGAGCGCTC 553
QY 484 GTGCGGTACTCATATATCCCGCTCAGCTGGCTCTCTTCTTCGATGATGATCGTCGACATTG 543
DB 552 CTCGCGGTGTACAGCGCGGCTGCGCGGGAGTTTACCGGCGAGTTCGAGCGGTTCAATG 493
QY 544 GGTCCCATCATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTGCACAACTTACCCCC 603

DB 492 GCGCGCGTCTCGAGCTTCTCTCGCGCGCACCGGCGGCGCGCTGCTCGCCAACTTACCCC 433
QY 604 TACTTGAAGCTATGCTGGCAACTCCGGATCCATCGACTCTCTCATACGCCCTCTTTACTGCA 663
DB 432 TACTTCTCTACACCTACAGCCAGGCGAGGTCGAGCTCTCTACGGGCTCTTACCGGC 373
QY 664 TCTGGTACAGTCTGTACAGGACCGGCTCTTACGCTTACAAACCTCTTTCGATGCGATGGTC 723
DB 372 GCGCGCACCGTCTGTCAGGACCGGCTTACGGGTACAGAACCTGTTCGACACCGCTC 313
QY 724 GACGATTTGTTACTTCGGCCCTGGAGAGCGCGGAGGCGCAATGTCTCTTGTCTGTCTG 783
DB 312 GACGCTTCTACGCGCCCATGGCCAAAGCACGCGCGCTCCGCGGTCTCTCTGCTCTCC 253
QY 784 GAGAGTGGCTGGCCCTGTCAGCGCGCGGAGCAGCGCGGACGCTGTCTAATGCGCAGACTTAC 843
DB 252 GAGACAGGCTGGCCCTCCGCGCGGCGCATGTCTCGCTCTGCGCGCCACGCCCGGATCTAC 193
QY 844 AATTCCAATTTGATCAACCATGTGGTTCAGGGGACGCGGAGAGGCGCAGGGGCGATTTGAG 903
DB 192 AACCAGAACCTCATCAACCCACGTCGCGCGCGGCGACGCGCGGCGCACCCCGCGCGCATCGAG 133
QY 904 ACCTACATATTTGCCATGTTTCAACGAGGATCAGAGGACGCCCAAGGGATTGAGATTAAC 963
DB 132 ACCTACGCTCTCTCTCATGTTCAACGAGAACCCAGAGGACGCG---CGGCGTCGAGCAGAAAT 76
QY 964 TTTGGGCTGTTTTCCTTACCTTAACGAGCCTGTCTATTTCGATCAGCTT 1010
DB 75 TGGGCGCTCTTTTACCCCAACATGACGACGCTTACCCCATCAGCTT 29

Search completed: April 7, 2006, 20:54:45
Job time : 718 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:27:54 ; Search time 5216 Seconds
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10091.156 Million cell updates/sec

Title: US-10-647-649-2

Perfect score: 1125

Sequence: 1 ttcatggcagctcagcacat.....ctaataaaactataaata 1125

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_hc:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

10: gb_gss2:*

11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435.2	38.7	1014	10	CL960506
2	410	36.4	1109	8	DR741429
3	392.8	34.9	1307	5	BUI03698
4	353.6	31.4	1005	10	CL971054
5	343	30.5	1107	7	CK210431
6	342.8	30.5	1025	7	CK162463
7	342.2	30.4	1014	10	CL960494
8	338.8	30.1	1134	7	CK161205
9	337.4	30.0	950	10	CG352135
10	335.6	29.8	1092	10	CL960507
11	335.4	29.8	1020	10	CL982353
12	328.2	29.2	1005	10	CL960504
13	327.6	29.1	927	10	CG450991
14	320.4	28.5	1005	10	CL960493
15	313.2	27.8	1017	10	CL959613
16	312	27.7	919	10	CG203193
17	307.4	27.3	764	5	BQ801977
18	304.8	27.1	1587	10	CL947558
19	303.2	27.0	4248	10	CL960511
20	302.6	26.9	823	7	CK201565
21	302.4	26.9	891	10	CM027959
22	301.6	26.8	840	6	CB673940

23	301.4	26.8	729	1	AJ613783
24	300.2	26.7	966	10	CL960877
25	299.6	26.6	858	8	CV766157
26	296.2	26.3	812	7	CK201895
27	296.2	26.3	1015	8	DR738420
28	295.4	26.3	781	9	CG646871
29	294.8	26.2	814	6	CB670194
30	292.8	26.0	751	2	BF265541
31	291.8	25.9	809	6	CB654106
32	291.8	25.9	861	6	CB644222
33	290.6	25.8	790	6	CF554537
34	290.6	25.8	1123	8	DR741036
35	290.4	25.8	817	6	CB670461
36	290.2	25.8	1033	7	CK214755
37	288.2	25.6	947	9	CG643933
38	288	25.6	790	6	CB653421
39	285.4	25.4	780	6	CB656551
40	285.4	25.4	805	6	CB657342
41	284.6	25.3	1096	8	DR739897
42	283	25.2	791	6	CB651782
43	283	25.2	828	6	CB670919
44	282.8	25.1	731	10	CL158546
45	282.4	25.1	790	6	CB652908

ALIGNMENTS

RESULT 1
CL960506
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CL960506 1014 bp DNA linear GSS 21-SEP-2004
OSIFCC004629 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
CL960506
CL960506.1 GI:52375716
GSS.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 1014)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1..1014
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match 38.7%; Score 435.2; DB 10; Length 1014;
Best Local Similarity 65.8%; Pred. No. 4.4e-107;
Matches 667; Conservative 0; Mismatches 338; Indels 9; Gaps 2;
Qy 4 ATGGCAGCTCAGCAGCATCATCTCCATGGCTCCATGCCATCCCTCTTGTAGTACTTCG 63
DB 1 ATGGCAAGCATGGTGTGTTTCATTTTAACTGGCATTTGCTTGGAGTACTTGGC 60

```
QY 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGGTCTGCAATGGAATGGACGGTGACAAACCTC 123
Db 61 GTCACTCCTCAAGTGTGTCATCCATTGGCGTGTGCTACGGCGTGAACCAACAACTG 120
QY 124 CCCAGCGCGCGAGCGTCAACTCTACAACTTCAAGTCCCAACATAGCTGGCATCGACTC 183
Db 121 CGGTGCGGAGGAGCGTGTGAAGCTCTACAGTCTGAAGGGGATCGATCCATGCGCATC 180
QY 184 TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACTCTCATCTC 243
Db 181 TACTTCCGAGGAGCGACATCTCCAGCGACTAAACGGCTCAACATCGCCCTCACCATG 240
QY 244 GAGTCCCACTCGACCTCCAAACATTTGGCTCTCGACCAATCGCGCGCCCAACCACTGG 303
Db 241 GGCGTCGCAACGAGAACTCTCGCGTTCGCTCCGACCCCTCCGCGTGGCCAAATTGG 300
QY 304 GTCCAAACCAACGTCACAGCTTACCACAAAGTGTGCTTCCGATACATCGCGTCGGAAC 363
Db 301 GTCAGAGAGACGTCCAGGTCTACCCGGCGGTCAACTTCCGCTACATCGCGTCCGCAAC 360
QY 364 GAAGTCATCCCGCGGCGCAAGCTCAGTACGTCTCTCCAGCCATGAAACAAACATACAGTCC 423
Db 361 GAGG---TTGAGAGCGCAACAGCGAGAACTCTCTCCGCGCATGCGAACAATGAACAGC 417
QY 424 GCGCTCTCTCTCGCGGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTCTCGGCGTC 483
Db 418 GCGCTCTCTCGCGGCTTCAGAACATCAAGGTCTCTCGTCTCGGTCTCCGACGAAGGCG 477
QY 484 GTCGTACTCTATATCCCGCTCAGCTGGCTCTCTCTCTCGATGATCGTCGACATTG 543
Db 478 GTGTCTCGCGGGTACCGCGGTTCATGGCATGTCTCTCTCCCGAAGCACTCTGATCATG 537
QY 544 GGTCCAAATACATACAGTTTCTAGCCAGCAATGGCTCCCACTTACTTGGCAACATCTACCCC 603
Db 538 ACGCCATCGGAGTACTCTGGGAGCACCGGCGCGCTGATGGCAACAGTCTACCCC 597
QY 604 TACTTGAGCTATGCTGGCACTCGCGATTCAT-----GACCTCTCATACGCGCTCTTT 657
Db 598 TACTTTCGCTACGTGGGCAACTCGCGGCGCCAGATCGACGACATCAACTAGCGCGCTCTTC 657
QY 658 ACTGCATCTGTACAGTCTACAGACGGGTCTTACGCTTACACCACTCTTCGATGCC 717
Db 658 ACGTCCCGGACAGTGTGTCGAGACGGCGAGAGGCTTACCAAGAACATGTTCGACGCC 717
QY 718 ATGTCTGACGCACTGTACTCGGCGCTCGAGAGCGCGGAGGCGCAATGTCTCTGTTGTC 777
Db 718 ATGTCTGACGCACTGTACTCGGCGCTCGAGAGCGCGGAGGCGTCCCGATCGT 777
QY 778 GTGTCGAGAGTGTGCGCGTACGCGGCGGAGACAGCGGCGACGCTGTCTAATGCGGAG 837
Db 778 GTGTCGAGAGCGGGTGGCGCTCGCGCGCGGCAACGCGGCGGAGCGCCAGCAACGCGCAG 837
QY 838 ACTTACAAATTCATCAACCTGCTGAGGAGCGCGGAGCGCGGAGGCGCGAGGCGG 897
Db 838 ACGTACAAACGAACTGATCAACACGTCGCGGAGGAGGAGCGCCCAAGAGCGCGGAGA 897
QY 898 ATTGAGACCTACATATTTGCAATGTTTCAACGAGGATCAGAGACGCGCCCAAGGATTCAG 957
Db 898 ATCGAGACCTACATTTTCGCCATGTTTCAACGAGAACGACAGAGAGGCGGAGAGCGGAG 957
QY 958 AATAACTTTGGGCTGTTTACCTTAACGAAACAGCGCTGTCTAATTCAGCTTC 1011
Db 958 AGGCACCTTCGGCTCTTCAACCGCTGATCAGTCGCGCGGCTCACCATTTAATTC 1011
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RESULT 2
LOCUS DR741429 1109 bp mRNA linear EST 18-JUL-2005
DEFINITION FGAS030484 Triticum aestivum FGAS: Library 2 Gate 3 Triticum
ACCESSION DR741429 aestivum cDNA, mRNA sequence.
VERSION DR741429.1 GI:70971098
```

KEYWORDS

SOURCE
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST.

Triticum aestivum (bread wheat)
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

1 (bases 1 to 1109)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress in Wheat and Canola Crops

Unpublished (2003)

Contact: Patrick Gulick

Plant Molecular Biology

Concordia University, Department of Biology

7141 Sherbrooke St. West, Montreal, Quebec H4B 1R6, Canada

Tel: 514 848 2424 Ext 3407

Fax: 514 848 2881

Email: pgulick@alcor.concordia.ca

This sequence is the direct result of the Base calling software
phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [37,809].

Plate: STG1 row: F column: 10.

Location/Qualifiers

1..1109

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial

parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite. This is the only library
that was done according to the Invitrogen manual, and
therefore, a percentage of clones will not have the 3
prime end because of NotI digestion within the cDNA."

ORIGIN

Query Match 36.4%; Score 410; DB 8; Length 1109;

Best Local Similarity 66.8%; Pred. No. 3.3e-100;

Matches 635; Conservative 0; Mismatches 301; Indels 15; Gaps 3;

QY 21 CATCTCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCGGCAATCCGAGGGGT 80

Db 66 CATGTTTTCGGTGGCGTGTGGCCCTTCTTGGAGTGTCTCTGGCATCCATTCCTACACGGT 125

QY 81 GGAATCCATTTGGGTCTGCAATGGAATGACGGGTGACAACTCCGCCAGCCGCGACGT 140

Db 126 GCACTTCATCGGCTGTGTCTACGGAGTGAACGGCGACGGCTTGCCTCGGCCGACGCT 185

QY 141 CGTCAACCTTCAAGTCCAAACAATAGTGGCATGCGACTCTACAGCCCGCCAGCAAGC 200

Db 186 CGTCAGCTCTTACAGTCCAAACGGCATCACGGCGATGCGCATCTACTTCCCGGACGCCAA 245

QY 201 CACTCTCAGGCCCTCCAGGGCTCTTAACATCTACTCTCTCGACGTCCCAACTCCGA 260

Db 246 GCGCTCGAGGCCCTCGAGCGCAGCAACATCGGCTCATCGCTGCGGCAACAGGGA 305

QY 261 CCTCAAAACATTGCTCCGACCAATCGCGCGCACCAACTGGGTCCAAACCAACGTCCA 320

Db 306 CTTGCTCTCCCTCGCTCCGACCGCTCGCGCGCACCGCTTGGTCCAGACCAACGTGCA 365

QY 321 AGCTTACCCAAACGTTGCTTTCCGATACATCGCGTCCGAAACGAAGT---CATCCCCGG 377

Db 366 GGCCTTACCGGGCTCAACATCAAGTACATCGCGCGCGGTAAACGAGGTGGGCGACGGG 425

QY 378 CGGCCAAGCTCAGTACGTCTCTCCAGCCATGAACAACATCAGTCCGCGCTCTCTCTGC 437

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426 CGCGCAGACGGGAAACATCTCCCGGCATGCGAACCTCGAGACCTCTCCGCGGC 485
438 CGGCTTTCAGAACATCAAGTCTCCACATCAGTCTCTTCGGCGTCTGGTACCTCAT 497
486 CGGCTCGCGGCGATCAAGTGTCCACGTCGGTCTCGAGGGCGTGACC---ACGGGTA 542
498 TCCCCCTCAGCTGGCTCTCTTCTTCGATGATCGTGCACATGGGTCCCAATACACA 557
543 CCTCTCCTCCCAAGGCACCTTCTCCGCG- - - - -GATACATGGGTCCCATAGCGCA 593
558 GTTCTAGCAGCAATGGCTCCCATATCTTGGCAACATCTACGCCCTACTTGAGCTATGC 617
594 GTACCTGGCCAGCACCGCGGCCCGCTGTCTGCGCAACGTGTACCCCTACTTCTCGTACGT 653
618 TGGCAACTCCGGATCCATCGACTCTCTATACGCGCTCTTTACTGATCTGGTACAGTGGT 677
654 GACAAACAGGCCAGATCGATCACTACGCGCTCTTTCAGTCTTCACGTGCGCGGCACCGTGT 713
678 ACAGGACGGGTCTACGCTTACAAACACCTCTTCGATGCCATGGTTCGACGCAATGTACTC 737
714 GCAGGACGGCGCAACCGGTACCAGAACCTGTTCGAGCGCTCTGTCGACACGTTCTACTC 773
738 GGCCTTGAAGAGCGCGGAGGGCGGAATGTCCCTGTGTGCTGTGTCGAGAGTGGCTGGCC 797
774 CGCGCTGAGAGCGCGCGCGCGGAGCGTCAACGTGTGTGTGTCGAAAGCGGGTGGGC 833
798 GTACGCGGCGGAGACAGCGCGGCGGAGCGTCAATCGGAGCTTACATTTCAATTTGAT 857
834 GTCCGCGCGGCGGACCGCGCGGCGGACACCGGACCGCGGAGAGCTCAACACGAACTGAT 893
858 CAACATGTGGTTCAGGGGACCGCGGAGGCGGAGGCGGAGGCTTGAGACTTACATATTGC 917
894 CNAACATGTGACAGGGGACCGCGGAGGCGGAGGCGGAGGCTTGAGGCGCTACGTGTGC 953
918 CATGTTCAACAGGATCAGAGACCGCGGAGGAGTGGAGATAAATTGG 968
954 CATGTTCAACAGGACAAAGGCGCGGCTGAGATCGAAAGCATTTGGG 1004
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```

RESULT 3
BU103698/c
LOCUS
DEFINITION
SCULRT1023E06.g Saccharum officinarum mRNA (Nogueira,F.T.S)
SOURCE
BU103698
ACCESSION
BU103698.1 GI:32815029
VERSION
EST.
KEYWORDS
Saccharum officinarum
ORGANISM
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE
1 (bases 1 to 1307)
AUTHORS
Nogueira,F.T.S., de Rosa,V.E. Jr., Menossi,M., Ulian,E.C. and
Arruda,P.
TITLE
RNA expression profiles and data mining of sugarcane response to
low temperature
JOURNAL
Plant Physiol. 132 (4), 1811-1824 (2003)
PUBMED
12913139
COMMENT
Contact: Nogueira FTS
Bioinformatics Lab
Organization for Nucleotide Sequencing and Analysis
C.P. 6176, Campinas, SP 13083-970, Brazil
Tel: 55 19 37881101
Fax: 55 19 37881089
Email: tebaldi@unicamp.br.
LOCATION/Qualifiers
1..1307
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
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/clone_lib="Saccharum officinarum mRNA (Nogueira,F.T.S)"
ORIGIN
Query Match
Best Local Similarity 34.9%; Score 392.8; DB 5; Length 1307;
Matches 645; Conservative 0; Mismatches 362; Indels 15; Gaps 2;
QY 4 ATGGCAGCTCAGCACATCATCTCCATGCTGCGATGGCATCCCTCTCTTGTAGTACTCTCG 63
DB 1222 ATGGCGAGCAGGGTGTGGCTTCCATGCTTGGCACTGGCATTTCTTCTCGAGCATTTGCA 1163
QY 64 GCAATCCGAGAGGCGTGGAAATCCATTTGGGCTTCGAATGGAAATGGACGGTGCACACCTC 123
DB 1162 GCAATTCCTACAGAGTGCAGTCCATCGCGGTGTGTACTCGGCGTGAAACGGCGACAATCTG 1103
QY 124 CCCAGCGCGCGCGAGCTGTCAACCTCTACAGTCCAAACACATAGTGGCATGGCATCGACTC 183
DB 1102 CGCTCGGCGAGCGAGCTGTGGTGAAGCTCTACCACTCCACGGCATCAACCTGTATGGCATC 1043
QY 184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTTAAACATCTACCTCATCTTC 243
DB 1042 TACTTCCCGGACACCAACGGCTCAACGGCTCAGCGGAGGAGCAACATCGGGTGTATCATG 983
QY 244 GACGTCCCAACTCCGACCTTCCAAACATTTGCTCCGACCAATCCCGCCCAACCAACTGG 303
DB 982 GACGTGCCCAACTCGGCCCTCTCTCGCTGGCCTCCGACCCGCGAGCGCGGCCACGCTGG 923
QY 304 GTCCAAACCAAGCTCAAGCTTACCAAAAGTGTGCTTCCGATATCATTCGCGCTCGGAAC 363
DB 922 GTGCAGAGCAACGTGCAGCGTTCCCGGGGGTCACTTCAAGTATCATCGCGCTGGGCAAC 863
QY 364 GAAGTATCCCGCGCGGCGGAGCTCAGTACGTCTCCAGCCATCAACCAACATACAGTCC 423
DB 862 GAGG---TCTCGGCGGGGATACCAACAGCATCTCTCCCGCCCATGCAACACGTCAACTCC 806
QY 424 GCCTCTCTCTGCGCGGCTTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTTCGCGCTC 483
DB 805 GCGTGCACCAACGCGGGCTGGGGAACATCAAGGTGTCCAGCGGTGCAGAGTGGGCTC 746
QY 484 GTGCTGACTCATATATCCCCCTCAGCTGGCTCTTCTCTTCGATGCTATGTCGACATG 543
DB 745 ACCCAGGGGTACCGCGCGCTCGCAGGGCAGCTTCTCGAGGGGTAC-----ATG 698
QY 544 GGTCAATCATACAGTCTTAGCCAGCAATGGCTCCCATTTACTTGCACATCTACCC 603
DB 697 GCGCCCATCGCGCAGTACCTTCAGAGCACGGGTGCCCCGCTCTCTGCAACGCTACCC 638
QY 604 TACTTGAGCTATGTGGCAACTCCGGATCCATCGACCTCTCATACGCTCTCTTACTGCA 663
DB 637 TACTTCTCTACCGGCAACGAGGCCAGATCGACCTCAGCTAGCGCTCTTCACTGCG 578
QY 664 TCTGTGATCAGTGTACAGGACGGGTCTTACGTTTACAAACACCTCTTCGATGCCATGTC 723
DB 577 TCGGAAACCGTGTGTCAGGACGGGCAACGCTACCAAGAACCTCTTCGACGCGCTCGTC 518
QY 724 GACCATTTGACTCGGCCCTGAGAGCGCGGAGGGCGGATGTCCTTGTGTGCTGTCG 783
DB 517 GACACCTTGTCTCGCGCTCGAGAACCGCGCGCGCGGGAACGTCGGCGTCTGTGTC 458
QY 784 GAGAGTGGCTGGCGCTCAGCGCGGGGACAGCGGCGAGCGGTGTCTTAATGCGCAGACTTAC 843
DB 457 GAGAGCGGGTGGCGCTGGCTGGCGGACCGCGCCACACCGGGGNAACGCGAGACTTAC 398
QY 844 AATTCCAATTTGATCAACCATGTGGTTCAGGGGACGCGGAGAGGAGCCAGGGCGGATTGAG 903
DB 397 AACCAGAACCTCATCAACCATGTGGGCGAGGCGCGCCCAAGCGCCCTGGAGCCATCGAG 338
QY 904 ACCTACATATTTGCAATGTTCAACGAGATCAGAGGACCGCGGAGGAGGATGAGATTAAC 963
DB 337 ACCTACATCTTTCGCTATGTTCAACGAGGACCGAGGAGCGGGAGCTGAGACGGAGGAC 278
QY 964 TTTGGCTGTGTTTACCTTACGAAACAGCTGTCTATTTCGATCAGCTTCTCACTTGGAAATT 1023
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Db 277 TTCCGACTTTTCAACCCGCAAAATCCCGCGGTACCCCAATCAATTTCTCTTAACAAGT 218
Qy 1024 TG 1025
Db 217 GG 216

RESULT 4
CL971054
LOCUS OSIRFCC021002 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL971054
VERSION CL971054.1 GI:52396716
KEYWORDS GSS
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1005)
Ma,L., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
Location/Qualifiers
1..1005
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match 31.4%; Score 353.6; DB 10; Length 1005;
Best Local Similarity 60.8%; Pred. No. 7.5e-85;
Matches 613; Conservative 0; Mismatches 389; Indels 6; Gaps 2;

Qy 4 ATGGCAGCTCAGCATCATCTCCATGGTGCATCCCTCTTGTAGTACTCTCG 63
Db 1 ATGGCTAGCCAAAGGTGTAGCTCCATGTCGCTCTCGCATGCTCTCGGTGCTTGGC 60

Qy 64 GCAATCCCGAGAGGGGTGAATCCATTGGGGTCTGCAATGGAATGGAGCGTGACAACCTC 123
Db 61 TCCATTCTCAAGCGGAGCGGATCGGGGTGTCTACGGATGAGCGCGGACCACTG 120

Qy 124 CCCAGCCCGCGAGCGTGTCAACCTTCAAGTCCAAACATAGCTGGGAGTCACTC 183
Db 121 CGCGCGGCGAGCTCGGTGTGGGGATGACCGCTCCACGGCATCACGTGATGGGCTG 180

Qy 184 TACAGCCCGGACCAAGCCACTTCCAGCCCTCCAGGGCTTCAACATCTACTCTCTC 243
Db 181 TACGCGCGGACGAGCGCGCTGAGTGGTGGGCGGACGGGATCAGCGTCTGCTC 240

Qy 244 GAGCTCCCAACTCCGACCTCCAAACATTGGCTCCGACCAATCCGCGCCACCACTGG 303
Db 241 GCGCGGCCCAAGAGTGTCTCCAACTCTGCGCGGCGGCGCGCGGCGGTCTGG 300

Qy 304 GTCCAAACCAAGCTCAAGCTTACCCAAAGTGTCTTCGAGATCATCGCGGTGGAAC 363
Db 301 GTGCGGAACAACATCAGCGCTTACCCTGCGGTGTGTTCCGGTACGTGCGCGTGGGAAC 360

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Qy 364 GAAGTATCCCGCGGCAAGCTCAGTACGTCTCTCCAGCATCAACAAACATACAGTCC 423
Db 361 GAGG---TCGCGGGGGGCGCCAGCTCCAGCTTGGTCCGCGGCATGGAGAAAGTCCGCGGC 417

Qy 424 GCGCTCTCTCTGCGGCGCTTTCAGAAATCAAGGTCTTCAATCAGTCTCTTTCGGCGTC 483
Db 418 GCGCTGTGTGCGGCGGCTGGGCGACATCAAGGTGACAGCTCGGTCTCGCAGCGCTC 477

Qy 484 GTGGGTACCTCATATCCCGCTCAGCTGGCTCTCTCTTCCGATGATCTCGACATTTG 543
Db 478 CTCGCGGTGTACAGCGCGCTGTCGCGCGAGTTTACCGCGAGTCCGAGCGGTTCATG 537

Qy 544 GGTCCAATCATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTGCACAAATCTACCCC 603
Db 538 GCGCGCGTCTGAGCTTCTGCGCGCACCGGCGGCGCTGCTCGCCAAATCTACCCC 597

Qy 604 TACTTGAGCTATGTGGCAACTCCGGATCCATTCAGACTCTCATACGCGCTCTTTACTGCA 663
Db 598 TACTTCTCTACACCTACAGCAGCGGAGCGTGCAGAGTCTCTTACGCGCTCTTACACGCG 657

Qy 664 TCTGGTACAGTCTCAGGAGCGGTCTTACGCTTACACAACTTTCGATGCCATGTC 723
Db 658 CCGCGCACCGTGTCTCAGGAGCGGCTTACCGGTACCCAGAACCTTGTTCGACACCACTGTC 717

Qy 724 GACGATTGTACTCGGCGCTGAGAGCGCGGAGCGCGGCGGCGGCTCGGTGTGTCGTCG 783
Db 718 GACGGTCTTACGCGCATGCGCAGCAGCGCGGCTCGGCGGCTCTGCTGTCTCTCC 777

Qy 784 GAGAGTGGCTGGCGCTCAGCGCGGCGGACAGCGCGGCGGCTCTTAATGCGCAGCTTAC 843
Db 778 GAGACAGGCTGGCGCTCGCGCGGCGGATGTCGCGCTCGCGCGCAACGCGCGGATCTAC 837

Qy 844 AATTCCAATTGTATCAACCATGTGGTTCAGGGAGCGGAGAGAGAGCGGCGGCGGATGAG 903
Db 838 AACCAGAACCTCATCAACCGTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 897

Qy 904 ACCTACATATTGTCATGTTCAACGAGGATCAGAGAGCGCGGCGGCGGCGGCGGCGGCGG 963
Db 898 ACCTACGCTTCTCATGTTCAACGAGACCGAGAGGAGCGC---CGGCGTTCGAGCGAAT 954

Qy 964 TTTGGGCTGTTTACCCTTAACGACAGCTCTCTTATTCGATCAGCTTC 1011
Db 955 TGGGCGCTCTTCTACCCCAACATGCGACGCTTACCCCATCAGCTTC 1002

RESULT 5
CK210431
LOCUS FGAS022241 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
DEFINITION aestivum cDNA, mRNA sequence.
ACCESSION CK210431
VERSION CK210431.1 GI:39572821
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticeae; Triticeae; Triticum.
1 (bases 1 to 1107)
Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_estes@cs.usask.ca

```

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [18,757].

Plate: L5B022 row: N column: 22.

FEATURES

source

Location/Qualifiers
1..1107

/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match 30.5%; Score 343; DB 7; Length 1107;
Best Local Similarity 63.3%; Pred. No. 6e-82;
Matches 556; Conservative 0; Mismatches 319; Indels 4; Gaps 2;

QY 4 ATGGGAGCTCAGACATATCTCCATGCTGCTGCGATCGATCCCTCTGTAGTACTCTCG 63
DB |||||
QY 109 ATGGGAGCTCAGGCTTCCCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
DB |||||
QY 64 GCAATCCCGAGAGGGGTGAATCCATTTGGGGTCTGCAATGGAATGGAAGGTGACAACTC 123
DB |||||
QY 169 TCCATCCCAAAAGCGTGAGTCCATCGAGTGTCTCGGATGAGCGGCAACACCTG 228
DB |||||
QY 124 CCGGAGCGCGGAGTGTGCTTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCA 183
DB |||||
QY 229 CCGGAGCGCGGAGTGTGCTTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCA 288
DB |||||
QY 184 TACAGCCCGGAGCGGAGTGTGCTTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCT 243
DB |||||
QY 289 TACGCCCCGACCGAGCGGCGCTGCGAGCGCGTGGCGGCGGCGGCGGCGGCGGCGGCG 348
DB |||||
QY 244 GAGCTCCCAACTCCGAGCTCCAAACATTTGCTCCGACCAATCCGCGCGCCCAACCACTGG 303
DB |||||
QY 349 GGGGCGCTTAAAGCTGTCTTCCAACTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 408
DB |||||
QY 304 GTCCAAACCAAGCTCAAGCTTACCCAAAGTGTCTTCCGATATCATCGCGTGGGAAC 363
DB |||||
QY 409 GTCCAGAGCAATCATCAGGCGCTTACCCCAAGTGTCTTCCGATATCATCGCGTGGGAAC 468
DB |||||
QY 364 GAGTATCCCGGCGGCGGAGCTCAGTACGCTCTCCAGGCGGCGGCGGCGGCGGCGGCGG 423
DB |||||
QY 469 GAGG---TGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525
DB |||||
QY 424 GCGCTCTCTCTGCGGCGGCTTCAGAACTCAAGTCTCCACATCATGCTCTCTTCTGCGGCTC 483
DB |||||
QY 526 GGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
DB |||||
QY 484 GTCCGATCTCATATCCCCCTTCAGTGTCTCTTCTTCCGATATCATCGCGTGGGAAC 543
DB |||||
QY 586 CTCGCGGTGTACAGCGCGGCTTCCGCGGCTCTTTCACGCGGAGGCGGCGGCGGCGGCG 645
DB |||||
QY 544 GGTCAATCATACATTTCTAGCAGCAATGGCTCCCATTTACTTGGCCAACTATACCCC 603
DB |||||
QY 646 GGACCTGTGGTGTCTTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 705
DB |||||

QY 604 TACTTGAGCTATGCTGGCAATCCCGATCCGATCCATCGACCTCTCATACGCGCTCTTTACTGCA 663
DB |||||
QY 706 TACTTGGCTGGGCTCTACAAACCGGAGCGCATGAGCATGAGCTACGCGCTCTTCANCGG 765
DB |||||
QY 664 TCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 723
DB |||||
QY 766 TCCGGCAACGCTGGGTCAGGACGGCTCTTACGCGGTACCGGATACCGGATGATGATGATGAT 825
DB |||||
QY 724 GACGATTTGATCTCGGCTCTGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 783
DB |||||
QY 826 GAGCGCTTCTACACGCGCATGCGGCGGCTCCAGCAGCGCGGCTCCAGCTGAGCTGATGATGAT 885
DB |||||
QY 784 GAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 843
DB |||||
QY 886 GANAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
DB |||||
QY 844 AATTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
DB |||||
QY 946 AA-CAGTACCTCATCAACCGATGCGGCGGCGGAGCGCGGAGCGCGGAGCGCGG 983
DB |||||

RESULT 6

CK162463

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

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FEATURES

source

1..1025

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;

Conditions for growth: Seeds were germinated in a

water-saturated mix (50% black earth and 50% ProMix) in a

growth chamber for 7 days under an irradiance of 200 mmol

m-2 sec-1. The temperature was maintained at 20 degrees C

with a 15-hr photoperiod under a relative humidity of 70%.

After this period watering of plants was stopped. Four

time points were sampled during a two week period; the

first after wilting was observed and the last, two weeks

later, consisted of live crown and leaf tissue (leaf

tissue that was yellow was not included in sampled

material). First strand synthesis in this library was done

in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN	Query Match Best Local Similarity Matches 531; Conservative 0; Mismatches 296; Indels 3; Gaps 1;
QY	4 ATGGCAGCTCAGCACATCATCTCCATGCTGCGATGGCATCCCTCTTGTAGTACTCTCG 63
DB	93 ATGGCGAGCCAAAGCGGTGCTCCATGTTGCTCTCGCATCTCTCGGGCCCTTCGCC 152
QY	64 GAAATCCCGAGAGCGGTGGAATCCATTCGGGTCTCGAATGGAATGGAGCGTGACAACTCTC 123
DB	153 TCCATCCCAACAAGCGTGGATCCATCGAGTGTCTAGCGCATGAGCGCCAAACACTTG 212
QY	124 CCCCACCGCGCGAGCGTGTCAACTCTTACAAGTCCAAACAATAGCTGGGATGCGACTC 183
DB	213 CCGCGGCGAGCACCGTGTGAGCATGTTCAAGTCCAAACGGCATCAACTCCATGCGGCTG 272
QY	184 TACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACTCTATCTTC 243
DB	273 TACGCCCGGACAGCGCGGTGTCAGCGCGTCCGCGGACCGGGTCAACGTGCTGCTC 332
QY	244 GACGTCCCAACTCCGACCTCCAAACATTTGCTCCGACCAATCCGCGCGCCACCAACTGG 303
DB	333 GGGCGGCTTACGACGTGTCTCCAACTCGCGCGAGCGCGCGCGCTCGTGG 392
QY	304 GTCCAAACCAAGCTCAAGCTTACCCAAAGTGTGCTTCGATATCATCGCGCTCGGAAC 363
DB	393 CTCAGGAGCAACATCCAGCGCTTACCCAAAGTCTCTCTCCGATAGTCTGCGTCCGCAAC 452
QY	364 GAAGTCATCCCGGCGGCGAGCTCAGTACGTCTCCAGCCATGCAACCAATACAGTCC 423
DB	453 GAGG---TCGCGGCGGCGGCCACCCAGAACTCTGTCGCGGCGCATGAAGACGTGCGGGC 509
QY	424 GCCTCTCTCTGCGCGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTCGGCGTC 483
DB	510 GGGCTGCGCTCGCTGGGTGGGCCACATCAAGGTCAACAGTCTGCGTGTGCGAGGCCATC 569
QY	484 GTCGGTATCTCATATCCCGCTTACGTGGCTCTCTTCTTTCGATGCAATCGTCGATTCG 543
DB	570 CTCGCGGTGTACAGCCGCGCTTCCGCGGCTCTTTCACCGGGAGCGGCGGTTCATG 629
QY	544 GTTCAATCATACAGTTTCTAGCCAGCAATGGCTCCCATTTACTTGGCCAAATCTACCCC 603
DB	630 GGACCGGTGGTGCAGTTCCTTGGCCGCAACCGCGCGCGCTCANGGCCAAACATCTACCCG 689
QY	604 TACTTGAGCTATGTGGCAACTCCGGATCCATCGACCTCTCATAGCGCTCTTTTACTGCA 663
DB	690 TACTTGGCTGGGCTTACACCCGAGCGCATGGACATGAGTACGCGCTCTTCAACCGN 749
QY	664 TCTGTTACAGTGTACAGAGCGGTCTTACGCTTACAAACACTTTCGATGCCATGTC 723
DB	750 GTCGGACCGTGGTCTCAGAGCGCTTCTACGGGTACCGAACTGTTCCAGCAACCCGCTG 809
QY	724 GAGCATTTACTCGGCTTGAGAGCGCGGAGCGGCGATGTCCCTGTTGTCGTGTCG 783
DB	810 GAGCGCTTCTACCGGNCATGCGCAAGCAGCGCGCTCCAAAGTGAAGCTGGTGTGTGTCN 869
QY	784 GAGAGTGGTGGCCGTTCAGCGGCGGCGAGCGGCGAGGTGTCTTAATGC 833
DB	870 GNAACCGGTGGGCGTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 919
RESULT 7	
CL960494	1014 bp DNA linear GSS 21-SEP-2004
LOCUS	CL960494
DEFINITION	OsIFCC004607 Oryza sativa Exress Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION	CL960494
VERSION	CL960494.1 GI:52375692
KEYWORDS	GSS.

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE	JOURNAL COMMENT	FEATURES	source
Oryza sativa (indica cultivar-group)				Class: exon-trapped.	Location/Qualifiers
Oryza sativa (indica cultivar-group)					1. 1014
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.					/organism="Oryza sativa (indica cultivar-group)"
1 (bases 1 to 1014)					/mol_type="genomic DNA"
Ma,L., Wang,J., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Jiao,Y., Sun,N., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Wong,G.K.S., Deng,X.W. and Wang,J.					/db_xref="taxon:39946"
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis					/clone_lib="Oryza sativa Exress Library"
Unpublished (2004)					/note="Oryza sativa exon trapped genomic sequences"
Contact: Chen Chen					
Department of Bioinformatic					
Beijing Institute of Genomics					
Chinese Academy of Sciences, Beijing 101300, China					
Tel: 86-10-80481559					
Fax: 86-10-80488676					
Email: chenchen@genomics.org.cn					
Rice genomic sequence.					
Class: exon-trapped.					
Location/Qualifiers					
1. 1014					
/organism="Oryza sativa (indica cultivar-group)"					
/mol_type="genomic DNA"					
/db_xref="taxon:39946"					
/clone_lib="Oryza sativa Exress Library"					
/note="Oryza sativa exon trapped genomic sequences"					
ORIGIN					
Query Match	30.4%;	Score 342.2;	DB 10;	Length 1014;	
Best Local Similarity	61.0%;	Pred. No. 9.7e-82;			
Matches	595;	Conservative 0;	Mismatches 368;	Indels 12;	Gaps 2;
QY	46	CTCTCTTGTGAGTCTCTCGGCAATCCGAGAGCGGTGGAATCATTTGGGGTCTGCAATGGA 105			
DB	49	CTTCTTGGAGTTTATCTCAATCCCTGTAGCGGTGCAATCCGTTGGTGTGTGTGTACGGC 108			
QY	106	ATGAGCGGTGACAACTCCCGAGCGCGCTCGTCAACCTCTCAACCTCTCAAGCTTCAAGTCCAACTCAAC 165			
DB	109	ATGATCGGCAACGATCTCCCGTCAAGAGCGACGTGCTGAGCTCTACAAATCCAAATGGC 168			
QY	166	ATAGCTGCGATGCGACTCTACAGCGCGGACCAAGCACTCTCCAGGCGCTCCAGGGCTCT 225			
DB	169	ATCAGACATGCGCATCTACTTCCCGACGTGAGGCGCATGAACGCTCTGGCGGCGACA 228			
QY	226	AACATCTACTCTCTCGAGCTCCCAACTCCGACCTTCCAAACATTTGCTTCGAGCCAA 285			
DB	229	GGCATCGGCTCTATCGTGGGTGCGCAACGACATCTCTCATCGACCTCGCGGCGCAACCGC 288			
QY	286	TCGCGCGCCCAACTGGTCCAAACGACGTCAGCTTCCAGCTTCCAGCTTCCAGCTTCCGA 345			
DB	289	CGCTCGCGCGGTCTTGGGTGCGCCAACTCAAGCGCTTCCAGCGCTTCCAGCGCTTCCGA 348			
QY	346	TACATCGCGGTGCGAAACGAAAGTCTATCCCGCGCGCCAAAGCTTCAAGCTTCCAGCGCTTCCGA 405			
DB	349	AAGTACATCGCGGTGCGCAACGAGATCTCCCGCGAGCCCAACGAGCAATCTCTCCGCTC 408			
QY	406	ATGAACAACTACAGTTCGCGCTCTCTCTGCGCGGCTTTCAGAAATCAAGGTTCTCCACA 465			
DB	409	ATGAGAACTCAACGCGCGCTTGGCGCGCGAGCATCACCGCGCTCAAGGCGTCCACG 468			
QY	466	TCAGTCTCTTGGGCGGTGCTGCTACCTCATATCCCCCTCAGCTGGCTCTCTCTTCC 525			
DB	469	CGGTGAAGCTAGACGTCTGTCACCAACGCTTCCGCGCTTCCGCGGCTGCTTCC----- 522			
QY	526	GATGCATCGTCGACATTTGGGTCCAATCATACAGTTTCTAGCGCAGCAATGGCTTCCCAATTA 585			
DB	523	---GGGCGGCTTACATGACGCGCGTGGCCAAAGCTCTCTGGGAGCAACCGCGCGCGCTG 579			
QY	586	CTTGCCAACTACTACCCCTACTTGAAGTATGCTGGCAACTCCGGATCATCGACCTCTCA 645			
DB	580	CTCGCCAACTACTACCCCTACTTGGCTTACATCGGCAACAAAGAGGACATCAGCTCTCAAC 639			


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Qy      844 A 844
Db      912 A 912

RESULT 9
CG352135
LOCUS   CG352135
DEFINITION  CG352135 950 bp DNA linear GSS 26-AUG-2003
          OGI:BTITV_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0726A22,
          genomic survey sequence.
ACCESSION  CG352135
VERSION    CG352135.1 GI:34269401
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 950)
          Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
          Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
          Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
          Consortium for Maize Genomics
          Other GSSs: OGI:BT11TH
          Unpublished (2002)
          Contact: Cathy Whitelaw
          TIGR
          7112 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TF
          Class: methylation filtered.
          Location/Qualifiers
            1..950
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /strain="B73"
              /db_xref="taxon:4577"
              /clone="ZMMBMA0726A22"
              /clone_lib="ZM 0.7 1.5 KB"
              /note="Vector: pBOSK; Site 1: HincII; 0.7-1.5 kb
              methylation filtered genomic DNA library"

FEATURES
             source
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ORIGIN
Query Match      30.0%; Score 337.4; DB 10; Length 950;
Best Local Similarity 61.9%; Pred. NO. 1.9e-80;
Matches 571; Conservative 0; Mismatches 346; Indels 6; Gaps 2;

Qy      75 AGGCGTGAATCCATTGGGGTCTGCAATGGATGACGGTGACACCTCCCGCCAGCCGC 134
Db      34 AGGTGCTAGAGCCATCGGGGTGTGCTACGGCATGAGCGCCCAACACCTGCCGGCGGCGAG 93
Qy      135 CGACGTCTCAACCTCTCAAGTCCAAACATAGCTGGCATGCGACTCTACAGCCCGGA 194
Db      94 CACGGTGTGAGCATGTAAAGCGCAACGGCATCTCGCGCATGCGGCTGTACGGCCGGA 153
Qy      195 CCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTCGACGTCCCA 254
Db      154 CCAGGGCGGTGCGAGCGGTGGGGCGGCACGGGCATCAGCTGGCGGTGGGGCGCCCA 213
Qy      255 CTCGACCTCCAAACATGTGCTTCGAGCAATCCGCGCCACCAACTGGGTCCAAACAA 314
Db      214 CGACGTGTCTCAACATCGGGGTAGCCCGCGCGCGCGCTGCTGGGTGCGCAACA 273
Qy      315 CGTCAAGCTACCCAAACGTGTGCTTCGAGTACATCGCGTCGGAACGAAGTCATCCC 374
Db      274 CATCAGGGGTACCCGTCGTGTCGCTACGTGTGCGTGGGCAACGAGG---TGGC 330
Qy      375 CGGCGGCCAAGCTCAGTACGTCTCTCCAGCCATGAAACATACATAGTCCGCCCTCTCTC 434
Db      331 CGGCGCGCGCGCAGGACCTTGGCGCGCCGCGCATGTGAGAACGTGCACGGCGCTGGCGC 390

FEATURES
             source
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               /organism="Oryza sativa (indica cultivar-group)"
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RESULT 11	CL982353	1020 bp	DNA	linear	GSS 21-SEP-2004
LOCUS	OsIFSC047411	Oryza sativa Express Library	Oryza sativa		
DEFINITION	cultivar-group) genomic, genomic survey sequence.				
ACCESSION	CL982353				
VERSION	CL982353.1	GI:52419188			
KEYWORDS	GSS.				
SOURCE	Oryza sativa (indica cultivar-group)				
ORGANISM	Oryza sativa (indica cultivar-group)				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
AUTHORS	1 (bases 1 to 1020)				
TITLE	Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Zhao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.				
JOURNAL	An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis				
COMMENT	Unpublished (2004)				
CONTACT	Contact: Chen Chen				
DEPARTMENT	Department of Bioinformatic				
INSTITUTE	Beijing Institute of Genomics				
CHINESE	Chinese Academy of Sciences, Beijing 101300, China				
TEL	Tel: 86-10-80481559				
FAX	Fax: 86-10-80488676				
EMAIL	Email: chenchen@genomics.org.cn				
RICE	Rice genomic sequence.				
CLASS	Class: exon-trapped.				
LOCATION	Location/Qualifiers				
FEATURES	1..1020				
SOURCE	/organism="Oryza sativa (indica cultivar-group)"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:39946"				
	/clone_lib="Oryza sativa Express Library"				
	/note="Oryza sativa exon trapped genomic sequences"				
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Query Match	29.8%;	Score 335.4;	DB 10;	Length 1020;	
Best Local Similarity	62.7%;	Pred. No. 6.9e-80;			
Matches	608;	Conservative 0;	Mismatches 346;	Indels 15;	Gaps 5;
Qy	58	CTCTCGGCAATCCGAGAGCGGTGGAAATCCATTGGGCTCGCAATGAATGACGGTGAC	117		
Db	46	CTGGCCCTCTCTCTCTGCGCACGTGCGGTGTCACCGGTGTTTGCTACGGCATGAACGGCGAC	105		
Qy	118	AACCTCCCCAGCGCCGCGACGTGCTCAACCTCTCAAGTCCAAACATAGCTGGCATG	177		
Db	106	AACCTCCCGTCGAGAGCGAGGTGTCGAGCTGTATCAAGTCCATGGTATCGTGTATG	165		
Qy	178	CGACTCTACAGCCCGCAACAGCCACTCTTCCAGGCCCTCCAGGGCTCTAACATCTACCTC	237		
Db	166	CGCATCTACAGCCCGGACCGAGCGCCCTCGACGGCTTCGCGGAGCGCGCTGCGCGTC	225		
Qy	238	ATCTCTGAGGT---CCCGAACTCCGACCTCGAAACATTTGCTCCGACCAATCCGCGGCC	294		
Db	226	ATCATCGAGTGGGGGCGAGCGCGGTGGCCACCTCGCCAAACACCCCTCCGCGGCC	285		
Qy	295	ACCACTGGGTCCMAACCAACGTCGAAGCTAC---CCAAAGTTGGCTTCCGATACATC	351		
Db	286	GCGAGTGGGTGGTGAACAGCTCAGGCTTACTGGCCGNAAGTATCATCCGGTACATC	345		
Qy	352	GCGGTCCGAAAAGAAAGTCAATCCCGCGGCCCAAGCTCAGTACGTCTCTCCAGCCATGAC	411		
Db	346	GCGGTCCGCAACAGAGCTCGGCCCGCGGACATGG---GGACCATCTCTCCCGGCCATGCAG	402		
Qy	412	AACATACAGTCCGCCCTCTCTCTGCGGCCCTTCAGAA---CATCAAGTCTCCACATCA	468		
Db	403	AACGTGTACGACGCGCTGTGTGTCGCGCGCCCTCTCGAACAGATCAAGGTGTGACGGCG	462		
Qy	469	GTCTCTCTCGGGTGTGTGGTACCTCATATCCCGCCCTCAGCTGGCTCTCTCTCTCCGAT	528		

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Db 463 GTGAGTGGAGCTGATCACCGCTCGTCCCTCGTGCAGCGGTGTTCCGCCGAC 522
Qy 529 GCATGTCGACATTTGGTGCATATACAGTTTCTAGCCAGCAATGGCTCCCAATTCTT 588
Db 523 CTGCAGCAGTTTCATGTTGCCATCGCGAGTTCTCTCGCCAAACACCATGTCGCCGTGCTC 582
Qy 589 GCCACATCTACCCCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 648
Db 593 GCCAACGTGTACCCCTACTTCCCTTACAGGACCAACCGCGGACATCCCGCTCAACTAC 642
Qy 649 GCCCTCTTTACTGATCTGTGTACAGTC---GTACAGGACGGGTCTTACGCTTACAAAC 705
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Qy 706 CTCCTTCGATGCGATGTCGACGCTATGCTGCGCCCTGGAGAGCGCGGAGGCGCGAAT 765
Db 703 CTCCTTCACGCGATGTTGACGCGCTGTACGCGCGCTGGAGAGGCGCGCGCGCGG 762
Qy 766 GTCCCTGTGTTGCTGCGAGAGTGGCTGGCGGCTCAGCGCGGCGGACAGCGCGACGGTG 825
Db 763 GTCCGCGCTGCTGCTGCGAGAGCGGTGGCGGCTGCGCGGAGGGTTTCGCGCGAAACGTG 822
Qy 826 TCTAATGCGCAGACTTACAAATTTCAATTTGATCAACATGTGGTTCAGGGGACGCCGAAG 885
Db 823 GAGAACGCGAGATCACACAGGGCGTGTGACACAGCTCAAGAACGGGACGCCGAG 882
Qy 886 AGGCGAGGGCGATGAGACCTACATATTTGCCATTTTCAACGAGGATCAGAAGCAGCG 945
Db 883 CGGCGCGGCGAGCTGGAGACGTACGTGTTCCGCTATTTCAACGAGAACCAAGACCGCGG 942
Qy 946 CAAGGATGAGATTAATTTGGCTGTTTACCTTACGACAGCCCTGCTATTTCGATC 1005
Db 943 GATGAGACCGAGAGCATTTTGGGCTCTTACCTGTACAGACGCGGCTTACCCGATT 1002
Qy 1006 AGCTTCACT 1014
Db 1003 AGCTTCTCT 1011

RESULT 12
CL960504
LOCUS CL960504
DEFINITION OsIFCC004627 Oryza sativa Expressed Sequence Library Oryza sativa (indica
VERSION CL960504
KEYWORDS cultivar-group) genomic, Expressed Sequence Library Oryza sativa (indica
SOURCE CL960504.1 GI:52375712
ORGANISM GSS.
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 1005)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
1..1005
/organism="Oryza sativa (indica cultivar-group)"
/mo_type="genomic DNA"
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/db_xref="taxon:39946"
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/note="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match 29.2%; Score 328.2; DB 10; Length 1005;
Best Local Similarity 61.9%; Pred. No. 6.3e-78;
Matches 630; Conservative 0; Mismatches 363; Indels 24; Gaps 6;

Qy 4 ATGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCG 63
Db 1 ATGCAGCACAGGGTGTACCTCGTGTAGCGGTGCTATTTGGTCACTCGAGCCTCTCGTG 60
Qy 64 GCATCCCGAGAGCGGTGGATCCATTTGGGTCTGCAATGCAATGGAGCGGTGACACCTC 123
Db 61 TCCATCCCTACA---GTGCAATCCATCGGCATGTGCTACCGCGGTGAAAGGAAACAACCTC 117
Qy 124 CCCAGAGCCGCGCAGCTCGTCAACTCTTACAAGTCCCAACATAGCTGGCATGCGACTC 183
Db 118 CCGCGCGGAGCGAGGTGGTGCAGCTGTACAAGTCCAAAGGCGCATCAACGGGATGGCATC 177
Qy 184 TACAGCCCGGACCAAGCCACTCTCCAGGCGCTCCAGGGCTCTAAACATCTACCTCATCTC 243
Db 178 TACTACCCCGACAGGAGGGGCTCAACGCCCTCGGCAACTCCGGCATCGCCTCATCTCTC 237
Qy 244 GAGTCCCGCAACTCCGAC---CTCAAAACATTTGGCTCCGACCAATCCGCGCGCCACCAAC 300
Db 238 GAGTCCCGCGGCTTTCGACACGGTGTCTATCTCGCGCGCAGCTCTCTCAACCGCGCGCG 297
Qy 301 TGGGTCCAAACCAACGCTC---CAAGCTTACCCCAACGTTTGGCTTCCGATCATCGCGCTC 357
Db 298 TGGGTCCGTGACACAGTCAAGGCCCTACTACCGCGCGCTCAACATCAGGTATCATGCGCTC 357
Qy 358 GGAACAGAGTCACTCCCGCGCGCAAGCTCAGTACGTCCTCCAGCGCATGAAACAACATA 417
Db 358 GGCAACGAGG---TGAAGAGCGCGCCAGCAATAGCATCTCTCCCGGCATCGCAACGCTC 414
Qy 418 GAGTCCCGCTCTCTCTCTCGCGGCTTTCAGAACATCAAGTCTCCACATCAGTCTCTCTTC 477
Db 415 AACTCCCGCTCTCTCTCTCGCGGCTTTCAGAACATCAAGGCTCCACCGCGCTGAAAGTTC 474
Qy 478 GGGCTCGTGGTACTCATATCCCGCTTACGCTGGCTCTCTCTCTTCGATGTCATCGCTCG 537
Db 475 GAGTCACTTCCAACTCTTACCCACCTCTCGCGCGCTCTTCAGGAGG-----CC 525
Qy 538 ACATTTGGGTCCAATCATACAGTCTTTCAGCCAGCAATGGCTCCCACTTACTTCCCAACATC 597
Db 526 TACATGAAGGACATCGCGGCTTACCTGGGAGCACCGCGCGCGCTGCTCGCTAAACGCTG 585
Qy 598 TACCCCTACTTTGAGCTATGCTGGCAACTCCGGATTCATCGACCTCTCATACGCGCTCTTT 657
Db 586 TACCCGTACTTTCGCTTACAGGGGGAACCGCGCGACATCAGCTCAACTACGCCACGTTTC 645
Qy 658 ACTGCATCTGTGACAGT---CGTACAGAGCGGTCTTACGCTTACCAACAACTCTTCGAT 714
Db 646 CGCGCGGCGCACCGTGGAGGAGCCCAACAAACCGGCTTCACTACACCACTGTTTCGAC 705
Qy 715 GCCATGTTGCAAGCATTTGTTACTTCGGCGCTTGGAGAGCGCGGAGGCGCGAATGTCCCTGTT 774
Db 706 GCCATGTTGCAAGCGCTGTACCGCGCTGGAGAGGCGCGCGCGGGAACGTTGAAGGTG 765
Qy 775 GTCTGTGCGAGAGTGGCTGGCGCTCAGCGCGCGGAGCAGCGGCGAGCGGTCTTAATCGG 834
Db 766 GTGGTGTGCGAGAGCGGGTGGCGCTCGCGCGGAGGGTTTCGGGGGAGCGGTGGAACAACG 825
Qy 835 CAGACTTACAAATTTGATCAACATGTGGTTCAGGGGACCGCGGAGCGGAGCGGCGAGG 894
Db 826 AGGGCGTACAAACAGGGGCTGATCGACCACTCGGGCGTGGCACGCCCAAGAGCGCGGG 885
Qy 895 GCGATTGAGACCTACATATTTGCCATGTTCAACGAGGATCAGAAGCAGCCCGCAAGGGATT 954
Db 886 CCACTGGAGGGGTACATATTTCGCCCATTTTCAGACGAGAACCAAGAGAGCGGGATCCCCACC 945
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QY 955 GAGNATAACTTTGGGCTTTTACCTTAACGACAGCCCTGTCTATTTCGATCAGCTTC 1011
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
946 GAGAAAAAATTTGGGCTCTCTTACCTTAACGACAGCCCTGTCTATTTCGATCAGCTTC 1002

RESULT 13
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DEFINITION genomic survey sequence.
ACCESSION CG450991
VERSION CG450991.1 GI:34835991
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
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/organism="Zea mays"
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methylation filtered genomic DNA library"

FEATURES
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Best Local Similarity 62.1%; Pred. No. 9e-78;
Matches 570; Conservative 0; Mismatches 339; Indels 9; Gaps 3;

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RESULT 14
CG450493
LOCUS OLSFCC004606 Oryza sativa Express Library Oryza sativa (indica
DEFINITION cultivar-group) genomic, genomic survey sequence.
ACCESSION CL960493
VERSION CL960493.1 GI:52375690
KEYWORDS GSS.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1005)
Jiao,Y., Wang,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
Ma,L., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
JOURNAL Department of Bioinformatic
COMMENT Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers
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/mol_type="genomic DNA"
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Search completed: April 7, 2006, 22:17:25
Job time : 5227 secs

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QY 433 TCTGCGGCTTTCAGAACATCAAGTCTCACAATCAGTCTCTTTCGGCGTCTGCGTACC 492
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RESULT 3

US-09-105-390-39
; Sequence 39, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455,30

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:

INFORMATION FOR SEQ ID NO: 39:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 912 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

NAME/KEY: Coding Sequence

; LOCATION: 1...912

OTHER INFORMATION:

US-09-105-390-39

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Best Local Similarity 67.0%; Pred. No. 3.3e-108;
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RESULT 4
US-08-457-797A-11
; Sequence 11, Application US/08457797A
; Patent No. 5689045
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; FILING DATE: June 1, 1995
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 18,839
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1050
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /codon start= 49
; OTHER INFORMATION: /function= "glucanase"
; OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1051..1235
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /note= "14 nucleotides at the 3' end not shown."
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1083..1088
; OTHER INFORMATION: /note= "potential polyadenylation signal"

; NAME/KEY: polyA_signal
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US-08-457-797A-11
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Best Local Similarity 60.4%; Pred. No. 2.le-89;
Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;
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RESULT 5

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; Sequence 11, Application US/08812025
; Patent No. 5804184
; GENERAL INFORMATION:
; APPLICANT: Transgenic pathogen-resistant organism
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brumbaugh, Graves, Donohue and Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,025
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tenser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
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; NAME/KEY: CDS
; LOCATION: 49..1050
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; NAME/KEY: polyA signal
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; OTHER INFORMATION: /note= "potential polyadenylation"
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; NAME/KEY: polyA_signal

; LOCATION: 1210..1215
; OTHER INFORMATION: /note= "potential polyadenylation"
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; NAME/KEY: mat_peptide
; LOCATION: 133..1050
; US-08-812-025-11

Query Match 30.8%; Score 346.2; DB 2; Length 1235;
Best Local Similarity 60.4%; Pred. No. 2.1e-89;
Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;
Qy 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTCTTAGTACTCTCG 63
Db 49 ATGGCTAGAAAGATGTTGCCTCCCATGTTGCAGTTGCTCTCTTATTGGAGCATTGCT 108
Qy 64 GCATCCCGAGAGGCGTGAATCCATGGGGTCTCAATGGGAATGGAGGTGCAACCTTC 123
Db 109 GCTGTTCTTACGAGTGTGCATCCATCGCGGTATGCTACGGCGTGTATCGGCAACACCTC 168
Qy 124 CCCAGCGCGCGAGCTGCTCAACCTCTACAGTCCAAACATAGTCCAAACATAGTGGCATGCGACTC 183
Db 169 CCTCCCGAGCGAGCTGTGTGAGCTCTACAGGTCCAAGGGCATCAACGGCATGCGCATC 228
Qy 184 TACAGCCCGGACCAAGCCACTCTCCAGGCGCTCCAGGGCTCTTAACATCTTACCTCATCTC 243
Db 229 TACTTCGCGGAGCGGCGAGCCCTCTCGGCGCTTCGCAACTCGGATCGGCTCTATCTC 288
Qy 244 GAGTCTCCCAACTCGGACTCTCAAAACATTTGCTTCGACCAATCCGCGCCCACTGCG 303
Db 289 GACATCGGCAACGACAGCTCGCAACATCGCGCGAGCACCTCCCAACGCGGCTCTCTGG 348
Qy 304 GTCCAAACCAACGTCCTCAAGCCCTTACCCAAACGTTGCTTCCGATACATCGCGTCCGAAC 363
Db 349 GTCCAGAAACAGCTGCGGCGCTTACTACCTCGCGTGAACATCAAGTATACATCGCCCGCGC 408
Qy 364 GAAGTCTATCCCGCGCGCAAGCTCAGTACGTCCTCCAGCCATCAACAAATACATAGTCC 423
Db 409 AACGAGGTGACAGGGGCGGCGCACGAGAGCATCTCGCGGCATCGGCAACCTCAACGGG 468
Qy 424 GCCTCTCTCTCGCGGCTTCAGAAACATCAAGGTCTCCACATCAGTCTCTCTCGGCGTTC 483
Db 469 GCGCTCTCGCGGCGGCGCTCGCGCCATCAAGGTGTCCACTCCATCGGTTCCAGCAG 528
Qy 484 GTCGTAACCTCATATCCCCCTCAGTGGCTCTTCTCTTCGATGATCTGTCGACATG 543
Db 529 GTGGCCAACTCTTCCCGCGCTCCGCGGCGTGTTCAGAAACGCTATACGACGACGCTG 588
Qy 544 GGTCAATCATACAGTTTCTAGCCAGCAATGGCTCCCGTCCCATTTACTTGCACCAATCTACCCC 603
Db 589 GCGCGGCTC-----CTGGCGAGCACCGCGGCGCGCTGCTCGCCAAAGTCTACCCC 639
Qy 604 TACTTGAGCTATGTGGCAACTCCGGATCCATCGACCTCTCATAGCCCTCTTTACTGCA 663
Db 640 TACTTCGCTACCGTGACAAACCCCGGGAGCATGAGCTTGAACCTAGCGACGCTTCCAGCG 699
Qy 664 TCTGTTACGT---CGTACAGGAGCGGTCTACGCTTACAAACAACTCTTCGATGCCATG 720
Db 700 GGCAACCGGTGCTGACCAACCAACCGGGAGCATGAGCTTGAACGCTGTTGTTGCTG 759
Qy 721 GTCCAGCATTTGTACTCGGCGCTCGAGAGCGCGGAGCGCGGCGGCTGTAAGCTGTTGCTG 780
Db 760 GTGGACCGCTGTACGGCGCTGGAGAGCGCGCGCGCGGCTGTAAGCTGTTGTTGCTG 819
Qy 781 TCGGAGAGTGGCTGGCGCTCAGCGGGCGGAGACGCGGCGAGCGGTGTCTTAATCGCAGACT 840
Db 820 TCGGAGAGCGGTGGCGCTCGGCGGCGGTTTTCGGCGCTCGCGCGCAATGCGCGGAG 879
Qy 841 TACAATTCATTTGATCAACCATGTGGTTCAGGGGAGCGCGGAGAGCGCGGCGGATTT 900
Db 880 TACAACGAGGGGCTGATCAACACACGTCGCGGGGCGGCGCGGCGGAGCGGCGCTG 939
Qy 901 GAGACCTACATATTGTCATGTTTCAACGAGGATCAGAAGCAGCGCGGAGGATTTGAGAT 960

Db 940 GAGACGTACATCTTCGCCATGTTCAACGAGAACAGAGACCGGGGACGCCACCGAGAGG 999
Qy 961 AACTTTGGGCTGTTTACCCTAAGAACAGAGCTGTCTATTGATCAGCTTC 1011
Db 1000 AGCTTGGGCTCTTCAACCCGAGCAAGTCGCGCGCATACACATCCAGTTC 1050

RESULT 6

US-09-138-873A-11
; Sequence 11, Application US/09138873A
; Patent No. 6271438
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic pathogen-resistant organism
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09138,873A
; FILING DATE: August 24, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Tenser, Arthur
; REGISTRATION NUMBER: 18,839
; NAME: Kole, Lisa
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Hordeum vulgare
; STRAIN: L.
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..48
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1050
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /codon start= 49
; OTHER INFORMATION: /function= "glucanase"
; OTHER INFORMATION: /product= "preprotein of the glucanase GluG"

; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1051..1235
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /note= "14 nucleotides at the 3'end not shown."
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 1083..1088
; OTHER INFORMATION: /note= "potential polyadenylation signal"
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 1210..1215

; OTHER INFORMATION: /note= "potential polyadenylation signal"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..1050
; US-09-138-873A-11

Query Match 30.8%; Score 346.2; DB 3; Length 1235;
Best Local Similarity 60.4%; Pred. No. 2.1e-89;
Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

Qy 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCG 63
Db 49 ATGGCTAGAAAAGATGTTGCTCCATGTTTGCACTTGTCTCTTCAITGGAGCATTCGCT 108
Qy 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGGTCTGCAATGGAATGGAGCGTGACAACCTC 123
Db 109 GCTGTTCTTACAGTGTGCAGTCCATCGCGTATGTACGGCGTGATCGGCAACCAACCTC 168
Qy 124 CCCAGCGCCGCGACGTCGTCAACCTCTACAAGTCCCAACACATAGCTGGCATCGACTC 183
Db 169 CCCTCCGAGAGCGACGTGGTGAGCTCTACAGTCCAGGGCATCAACGGCATGGGCATC 228
Qy 184 TACAGCCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTC 243
Db 229 TACTTCCGAGCGGCGAGGCCCTCTCGCGCGTCCGCAACTCCGGCATCGGCTCATCTC 288
Qy 244 GAGTCCCGCAACTCCGACCTCCAAAACATTGGCTCCGACCAATCCGGCGCCACCACTGG 303
Db 289 GACATCGGCAACGACAGCTCGCCAAACATCGCCCGACACCTCCAAACGGCGCTCTCTGG 348
Qy 304 GTCCAAACCAACGTCCTCAAGCCTACCCAAAGCTTCCCTTCCGATACATCGCGTCGGAAAC 363
Db 349 GTCGAGAACACGTCGGCGCCCTACTACCTGCGGTGAACATCAAGTACATCGCGCGGC 408
Qy 364 GAAGTCTATCCCGCGCGCCAAAGCTCAGTACGTCTCCAGCATGAAACAAACATACAGTCC 423
Db 409 AACGAGGTGCAGGCGCGCGCCAGCAGAGCATCTCGCGCGCATGCGCAACTCAACGCG 468
Qy 424 GCCCTCTCTCTCGCGCGCTTCAGAAATCAAGTCTCCACATCAGTCTCTTTCGGGCTC 483
Db 469 GCCCTCTCTCGCGCGCGGGCTCGGGCCATCAAGGTGTCCACCTCATCTCCGTTTGACGAG 528
Qy 484 GTCGGTACCTCATATCCCCCTCAGCTGGCTCTTCTTCCGATGATCGTCGACATG 543
Db 529 GTGGCAACTCTTCCCGCCCTCGCGCGGTGTTCAGAACGCTCATACAGCGACGTG 588
Qy 544 GGTCCAAATCATACAGTCTTCTAGCCAGCAATGGCTCCCAATTTCTTGCACATCTACCCC 603
Db 589 GCCCGGCTC-----CTGGCGAGCACCGCGCGCGGTGCTCGCCAAAGTCTACCCC 639
Qy 604 TACTTGAGCTATGCTGGCAACTCCGGATCCATGACCTCTCATAGGCCCTCTTTACTGCA 663
Db 640 TACTTCGCTACCGGTGACAAACCCCGGAGCATAGCCTTGAACTAGCGACGTTCAGCGCG 699
Qy 664 TCTGTACAGT---GCTACAGAGCGGTCTTACGCTTACAAACACTCTTCGATGCCATG 720
Db 700 GGCACACCGTGCCTGACCAAGAACAAACGGGCTGACTACAGCTCCCTGTTGACGCGATG 759
Qy 721 GTCGACGCAATTGTACTCGGCCCTTGAGAGCGCGGAGGCGCAATGTCCCTGTTGTCTGTG 780
Db 760 GTGGAGCGCGGTGTACGGGGCTGAGAAAGCCGCGCGCGGTGAAGTGTGTGTG 819
Qy 781 TCGGAGAGTGGCTGGCGGTGAGCGGGGAGACAGGGGAGCGGTGTCTAATGCCGAGACT 840
Db 820 TCGGAGAGCGGGTGGCGGTGCGCGCGGGGTTCGCGGTGCGCGCGCAATGCGCGGAGC 879
Qy 841 TACAATTCCAATTTGATCAACCATGTGGGTGAGGGAGCGCCGAAAGAGCCAGGGCGCAT 900
Db 880 TACAAACAGGGGCTGATCAACACAGTTCGCGGGGGACGCCCAAGAGCGGGAGCGGTG 939
Qy 901 GAGACCTACATATTTTGGCATGTTCAACAGAGATCAGAAAGACCGCCAAAGGATTCAGAA 960
Db 940 GAGACGTACATCTTCGCCCATGTTCAACGAGAAACAGAGACCGGGGAGCGCCACGAGAGG 999

QY 961 AACTTTGGGCTGTTTACCTTAACGAAACAGCCCTGTCTATTTCGATCAGCTTC 1011
DB 1000 AGCTTCGGGCTCTTCAACCGGACAGTCCGGGCATACCAACATCCAGTTC 1050

RESULT 7

US-09-105-390-57
; Sequence 57, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; TITLE OF INVENTION: and Genes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: Fast-Seq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; FILING DATE: Filed herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; FILING DATE: 60/050,675

; ATTORNEY/AGENT INFORMATION:

; NAME: Petichory, Joanne R.

; REGISTRATION NUMBER: P42,995

; REFERENCE/DOCKET NUMBER: 2000-0455.30

; TELEPHONE: 650-324-0880

; TELEFAX: 650-324-0960

; TELETYPE:

; INFORMATION FOR SEQ ID NO: 57:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 996 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1...996

; OTHER INFORMATION:

US-09-105-390-57

Query Match 29.4%; Score 330.6; DB 3; Length 996;
Best Local Similarity 61.4%; Pred. No. 6e-85;
Matches 607; Conservative 0; Mismatches 364; Indels 18; Gaps 4;

QY 29 TGGCTGCATGCGATCCCTCTTGTAGTACTCTCGGCAATCCGAGAGCGGTGGAATCCA 88
DB 17 TTGCTCCCGTGTGTCAGTAGCATTTGCTTGCAGCATTTCTCGACGGGTTCAGTCCA 76
QY 89 TTGGGGTCTGAATGGAATGACGCTGACACCTCCCGAGCCCGCGCTGCTCAACC 148
DB 77 TTGGGGTGTCTACGGGTGATCGGCAACAACTTGCAGCGCGAGCGAGCTGCGAAGC 136
QY 149 TCTAAGTCAACAAACATAGTGTGCGATGCGACTCTACAGCCCGCCGACCAAGCACTCTCC 208
DB 137 TCTAAGTCCAAAGGGATCGACTCCATGCGCATCTCTTCCGAGGAGCGACATCTCC 196
QY 209 AGGCCCTCCAGGGCTCTTAACATCTACCTCGAGCTCCCAACTCCGACCTCCAAA 268
DB 197 AGGCACTCAGCGGCTCGAACAATCGCCCTCACCATGAGCTCGCCAAACGAGAACCTCGCG 256

QY 269 ACATTTGGCTTCGACCAATCCGCGCCACCAACTGGTCCAAACCAAGCTTCAAGCTTACC 328
DB 257 GTTCCGCCCGGAGCGCCACCGGCGGGTGGGTGAGTCAAGCAGAACGCTTCAAGGCTTACC 316
QY 329 CAAAGTTGGCTTCGATATACATCGCGCTCGGAAACGAAAGTCAATCCCGCGCGCTTCAAG 388
DB 317 CGGGGCTCTCTTCCGCTACATCGCGCTCGGCAACGAGGTCA--CCGCGCAGCAGCACGG 373
QY 389 AGTACGTCTCCAGCCATGAACACATACAGTCCGCTCTCTCTCTGCGGGCTTCAAG 448
DB 374 GCAACATCTCCCGCCATGAAGAACCTCAACCGCGCTCGCGCGCGCTCGGCTCGGG 433
QY 449 ACATCAAGGTCTCCACATCAGTCTCTTCCGGGTGCTGCGTACCTTCAATATCCCGCTCAG 508
DB 434 GGTTCGGGGTGTGAGCTGCTGCTGCTCCAGGGGTGATCGCCAACTCTTACCGCTTCCA 493
QY 509 TTGGCTCTCTTCTTCGATGCAATCGTCCGATTCGAGTTCGAGTTCGATATACAGTTTCTAGCCA 568
DB 494 ACGGGTCTTCAACGACGACTAC-----ATGTTTGACATCGTGGAGTACCTGGCGA 544
QY 569 GCAATGGCTCCCATTTACTTGGCAACATCTACCCCTACTTGAAGTATGCTGGCAACTCCG 628
DB 545 GCACCGGAGCGCGCTGCTGCTGTTAACTGTTACCTTACCTTACCTTACCTTACCTTACCT 604
QY 629 GATCATCGACCTCTCATACGCGCTCTTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
DB 605 AAGACATCAGCTTCACTACGCGCTTCCAGCGCGGCGACGAGCGGCTGAGCGAGCGCA 664
QY 689 CC---TACGCTTTACAAACACCTCTTTCGATGCGCATGCGTTCGAGCTTGTACTCGGCTCGG 745
DB 665 GCGGCTGATCTACACGAGCTCTTTCGACGCGATGCTGATTCCTCTTACGCGCGCTCG 724
QY 746 AGAGCGCGGAGCGCGAATGCTCCCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 805
DB 725 AGGACGCGCGCGCGCGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784
QY 806 GCGGACAGCGCGAGCGCTGCTAATGCGAGACTTACAAATTCGAATTCGAATTCGAATTCGA 865
DB 785 GTGGTTTCGGGGCGCGCTGAGCAACGCGCGAGACTCAACGAGAGCTTATCAGCCATG 844
QY 866 TGGGTTCAGGGGACCGCGAAGAGCGCGAGG---GGCGATTGAGACCTTACATATTTGCCATGT 922
DB 845 TCCAAGGAGGCACTCCGAGAGAGCAGCGGTGGGTTCGAGAGCTGCTGCTGCTGCTGCTGCT 904
QY 923 TCAAGAGGATCAGAGCAGCGCGAGAGGATGAGAAATAATTTGGGCTGTTTACCTTA 982
DB 905 TCAACGAGAACCGAGAGACCGGGGTGAGACCGAGAGGCACTTTCGGGCTGTTTCAACCCCA 964
QY 983 ACGACAGCTGCTTATTCGATCAGCTTC 1011
DB 965 ACAAAGTCCGCTCTTACAAATTTAGATTTC 993

RESULT 8

US-09-105-390-5
; Sequence 5, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; TITLE OF INVENTION: and Genes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/105,390
/ FILING DATE: Filed herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/050,675
/ FILING DATE: 25-JUN-97
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Petithory, Joanne R.
/ REGISTRATION NUMBER: P42,995
/ REFERENCE/DOCKET NUMBER: 2000-0455.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
/ TELEFAX: 650-324-0960
/
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2169 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-09-105-390-5
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Query Match 28.9%; Score 325; DB 3; Length 2169;
Best Local Similarity 62.1%; Pred. No. 3.7e-83;
Matches 587; Conservative 0; Mismatches 340; Indels 18; Gaps 4;

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QY 73 AGAGCGGTGGAAATCCATTGGGTCTGCAATGGAATGAGCGGTGACAACTCCCCAGGCC 132
Db 1231 ACAGCGGTTCAGTCCATTGGGTGCTACGGCGTATCGGCAACAACCTGCGCGGG 1290
QY 133 GCGGAGGTGCTCAACTCTCAAGTCCCAACAACTAGCTGGCATCGGACTCTACAGCCCC 192
Db 1291 AGCGACGTGCTGAAGCTCTCAAGTCCCAAGGGAATCGACTCATCGCATCTACTTCCCG 1350
QY 193 GACCAAGGCACCTCTCAGGCGCTCCAGGCTCTACATCTACCTCATCTCGAGCTCCCC 252
Db 1351 AGGAGGACATCTCTCAGGACATCTACGGCTCGAATCGGCTCACCATGAGAGCTGCC 1410
QY 253 AACTCCGACCTCAAAAACATTCCTCCGACCAATCCGCGCCACCAACTGGGTCCAAACC 312
Db 1411 AACGAGACCTCGCGGTTCGCGCGGACGCAACCGCGCGGTGCGTGGGTCAAGCAG 1470
QY 313 AACGTCGAAGCTTACCCAAAGCTTCCGATCATCGCGGTGCGGAAACGAAGTCAATC 372
Db 1471 AACGTCCAGGCTTACCGGCGCTCTCTTCCGCTACATCGCGGTGCGCAACGAGGTCA-- 1528
QY 373 CCGGCGGCGCAGCTCAGTACGTCTCCGCGCATGACACATACAGTCCGCGCTCTCC 432
Db 1529 -CGGCGGAGGACACGCGGCAACATCTCCGCGCATGAGAACCTCAACGCGCGCTCGGC 1587
QY 433 TCTGCGGCGCTTCAGAAACATCAAGGTCTCCATCAGTCTCTCTCGGCGTCTCGGTACC 492
Db 1588 GCGGCGGCGCTCGGCGGTGCGGTGTCGAGTCTCGGTGCCAGGGGTGATCGCCAAAC 1647
QY 493 TCATATCCCCCTCAGCTGGCTCTCTCTTCCGATGATCGTGCATATGGGTCAATC 552
Db 1648 TCTTACCGCGCTTCCAAAGCGGCTCTTCAACGACGA-----CTACATGTTTGACATC 1698
QY 553 ATACAGTTTCTAGCAGCAATGGCTCCCATTTACTTGGCCACATCTACCCCTACTTGAGC 612
Db 1699 GTGGAGTACTTGGCAGCAGCGGCGCGCTGCTGGTAAAGGTATACCCCTACTTCCGC 1758
QY 613 TATGCTGGCAACTCCGGATCCATGACCTCTCATACGCGCTCTTTACTGCACTCTGGTACA 672
Db 1759 TACGTGCGGACACGAAAGACATAGCTCAACTACGCAAGCTTCCAGCGGGGACGACG 1818
QY 673 GTCTGACAGGAGGCTCTTACGCT---TACAAACACTCTTTCGATGCGATGTCGAGCA 729
Db 1819 GTGACGAGGACGCGGAGGCGGTGATCTACAGAGCTCTTTCGACGCGATGCTGATTC 1878
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RESULT 9

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US-09-105-390-41
; Sequence 41, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Petithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
;
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; NAME/KEY: Coding Sequence
; LOCATION: 1...921
; OTHER INFORMATION:
/
/ US-09-105-390-41
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Query Match 28.4%; Score 319.6; DB 3; Length 921;
Best Local Similarity 62.2%; Pred. No. 8.5e-82;
Matches 578; Conservative 0; Mismatches 334; Indels 18; Gaps 4;

Db 469 GCGGTGAAGCTAGAGCTGTCACCAACAGTTCGCGGCTCGCGGGTGTTC----- 522
Qy 526 GATGATCGTCGACATTTGGTCCAAATACATACAGTTTTCAGCAGCAATGGCTCCCAATTA 585
Db 523 ---GCGGCGCTTACATGACGGCGGTGGCCAAAGCTCTCTGCGATGCACCGGCGCGCGTG 579
Qy 586 CTTCGCAACATCTACCCCTACTTGAAGCTATGCTGGAACCTCGGATCCATCGACTCTCA 645
Db 580 CTCGCCAACATCTACCCCTACTTGCCTTACATCGGCAACAAAGAGGACATCAGCCTCAAC 639
Qy 646 TACGCGCTCTTTACTGTCATCTGGTACAGCTCGTACAGGACGGTCTCTAC---GCTTACAA 702
Db 640 TACGCGAGTTCAGGCGCGGACAGCGGTGCGGCCGACCCCAACACAGACTGTGTAGCC 699
Qy 703 AACCTCTTCGATGCCATGGTCGACGATTTGTAATCTCGGCTTCGAGAGCGCGGAGGCG 762
Db 700 AACCTGTTCGAGCGCATGTCTGACTCGCTTACGCGCGCTGGACAAGGCGCGCGCG 759
Qy 763 AATGTCCTGTGTGTCGAGAGTGGCTGGCGCTCAGCGGGGAGACAGCGCGGACG 822
Db 760 GCGCTCAGCATCGTGTGTCGAGAGCGGCTGGCGCTCGGCGCGGCGGACTCGGCCACG 819
Qy 823 GTGTCTAATGCGCAGACTTACAAATTTCCAAATTTGATCAACCATGTGGTTCAGGGACGCG 882
Db 820 ATCGACATCGCGCGGACCTTACGTGAGAACCTGATTAAGCATGCGAAGAGGGGACGCG 879
Qy 883 AAGAGCGCGGCGGATTTAGACCTTACATATTTGCCATGTTTCAACGAGGATCAGAAGCAG 942
Db 880 AA---GCCGGGTGATCGAGACGTACGTGTCGCCATGTTCAACGAGAACGAGAGGCC 936
Qy 943 CGCAAGGGATGAGAAATTAATTTGGGCTGTTTACCCCTAACGACAGCCTGTCTATTTCG 1002
Db 937 GGGGAAGCAGCGGACAAATTTTGGAGCCTTCTACCCCTAACAGACAGCAGTCTACCC 996
Qy 1003 ATCAGCTTC 1011
Db 997 ATCAATTC 1005

RESULT 11

US-09-105-390-2

Sequence 2, Application US/09105390

Patent No. 6288303

GENERAL INFORMATION:

APPLICANT: Rodriguez, Raymond

TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: and Genes

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESS: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/105,390

FILING DATE: Filed herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/050,675

FILING DATE: 25-JUN-97

ATTORNEY/AGENT INFORMATION:

NAME: Petichory, Joanne R.

REGISTRATION NUMBER: P42,995

REFERENCE/DOCKET NUMBER: 2000-0455.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1949 base pairs

TYPE: nucleic acid

STRAINEDNESS: single

TOPOLOGY: linear

US-09-105-390-2

Query Match 27.6%; Score 310; DB 3; Length 1949;

Best Local Similarity 60.4%; Pred. No. 7.4e-79;

Matches 571; Conservative 0; Mismatches 360; Indels 15; Gaps 3;

Qy 75 AGCGTGGAAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCCAGCCGCG 134

Db 1016 AGCGTGGAAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACAACTCCCCAGCCGCG 1075

Qy 135 CGAGCTGTCMACTCTTACAAAGTCCAAACATAGCTGGCATGCGACTCTACAGCCCGA 194

Db 1076 CGAGCTGTCMACTCTTACAAAGTCCAAACATAGCTGGCATGCGACTCTACAGCCCGA 1135

Qy 195 CCAAGCCACTCTCCAGGCGCTCCAGGCGCTTAAACATCTTACCTCATCTCGACGTCGCCAA 254

Db 1136 CGTCAAGCCACTCTCCAGGCGCTCCAGGCGCTTAAACATCTTACCTCATCTCGACGTCGCCAA 1195

Qy 255 CTCCGAGCTCCMAAACATTTGCTCCGACCAATCCGCGCCCAACCAACTGGGTCCAAACCAA 314

Db 1196 CGACATCTCATGACCTCGCGCGCAACCGCGCGCTCCGCGCGCTCCGCGCGCTCCGCGCG 1255

Qy 315 CGTCAAGCTTACCCAAAGCTTGGCTTCGATATCATCGCGTTCGGAACAGAGTCAATCCC 374

Db 1256 CGTCAAGCTTACCCAAAGCTTGGCTTCGATATCATCGCGTTCGGAACAGAGTCAATCCC 1315

Qy 375 CGCGGCGCAAGCTCAGTAGCTCCCTCCAGCCATCAACAAATAGTCCGCGCTCCGCGCT 434

Db 1316 CGCGGCGCAAGCTCAGTAGCTCCCTCCAGCCATCAACAAATAGTCCGCGCTCCGCGCT 1375

Qy 435 TGCGGCGCTTCAGAACATCAAGGTCTCCACATCATCTCTTCGCGCGCTTCGCGCTTC 494

Db 1376 GCGGAGCATCACCGGCTCAAGGCGTCCACGGCGTGAAGCTAGACGCTCGTCAACCAAC 1435

Qy 495 ATATCCCGCTCAGCTGGCTCTCTCTTCGATGATCGTTCGATGATGATGATGATGATGAT 554

Db 1436 GTTCCCGCTTCGCGCGCGCTGTTT-----GCGCGCGCTTACATGACGCGCGTGGC 1486

Qy 555 ACAGTTTCTAGCCAGCAATGGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 614

Db 1487 CAAGCTCTGCGATGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1546

Qy 615 TGCTGGCAACTCCCGATCCATCGACCTCTCATAGCGCTCTTTACTGATCTGGTACAGT 674

Db 1547 CATCGGCAACAAAGAGGACATCAGCTCAACTAGCGCGCTTCCAGGCGCGGACGACGCT 1606

Qy 675 GGTACAGGACCGGCTCTTAC---GTTTACAAACAACTCTTCGATGCGCATGCTGCGAGCT 731

Db 1607 GCGGACCGGCTCTTAC---GTTTACAAACAACTCTTCGATGCGCATGCTGCGAGCT 1666

Qy 732 GTACTCGGCGCTGAGAGCG 791

Db 1667 CTACGCGCGCTGAGAGCG 1726

Qy 792 CTGGCGCTGAGCGCGCGGACAGCGCGGACGCGTGTCTAATGCGGAGCTTCAATTCGAA 851

Db 1727 GTGGCGCTGAGCGCGCGGACAGCGCGGACGCGTGTCTAATGCGGAGCTTCAATTCGAA 1786

Qy 852 TTTGATCAACATGTTGGTTCAGGGGACCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 911

Db 1787 CCTGATTAAGCATGCGAAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1843

Qy 912 ATTTGCCATGTTCAACGAGGATCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 971

Db 1844 GTTCGCCATGTTCAACGAGAACCCAGAGAGCCCGGGAGAGCCAGGAGCAAAACTTTGGAGC 1903
QY 972 GTTTTACCCTAACGAGACACCGCTGTCTATTTCGATCAGCTTCACTTGA 1017
Db 1904 CTTTACCTTAACAGACAGCAGTCTACCTTATCAATTTCCAGTGA 1949

RESULT 12

US-09-105-390-35
; Sequence 35, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond

; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/105,390

; FILING DATE: Filed herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/050,675

; FILING DATE: 25-JUN-97

; ATTORNEY/AGENT INFORMATION:

; NAME: Pettichory, Joanne R.

; REGISTRATION NUMBER: P42,995

; REFERENCE/DOCKET NUMBER: 2000-0455,30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-324-0880

; TELEFAX: 650-324-0960

; TELEX:

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 918 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Coding Sequence

; LOCATION: 1..918

; OTHER INFORMATION:

US-09-105-390-35

Query Match 26.5%; Score 298; DB 3; Length 918;
Best Local Similarity 60.0%; Pred. No. 1.4e-75;
Matches 556; Conservative 0; Mismatches 355; Indels 15; Gaps 3;

QY 89 TTGGGCTGCAATGGAATGACGGTGACAACTCTCCCGCCGACCGCGTCTCAACC 148
Db 2 TTGGTGTGTGTAGCGCATGATCGGCAACGATCTCCCGTCGAAGAGCGACGTCGTGCAGC 61
QY 149 TCTACAGTCCCAACACATAGCTGGCATGCGGATCTACAGCCCGCCGACCAACGCACTCTCC 208
Db 62 TCTCAAAATCAATGGCATCAACAGATGCGCATCTACTTCCCGGACGTCGAGGCCATGA 121
QY 209 AGGCGCTCCAGGCTCTAACTATCTACCTCATCTCGAGCTCCCACTCCGACCTCCAAA 268
Db 122 ACGCCCTGGCGGACAGGATCGGCTCATCTGTCGGGTGCGCAACGACATCTCTCATCG 181
QY 269 ACATTGCTCCGACCAATCCCGCCGACCAACTGGGTCCAAACCAACGTCGCAAGCCTACC 328

Db 182 ACCTCGCGCCCAACCCGCGCTCCGCGCGTCTCTGGTTCGACGCAACGTCGAAGCCGTTGC 241
QY 329 CAAAGCTTTCCTTCGATACATCGCGCTCGGAAACGAAGTCATCCCGCGCGCCAGCTC 388
Db 242 TCCCGCGGTGAAATCAAGTACATCGGAGTCGGCAACGAGATCTCCGCGGAGCCACGC 301
QY 389 AGTACGTCTCCAGCCATGAACAATACATACAGTCCGCCCTCTCTCTGCGGCGCTTCA 448
Db 302 AGAATCATCTCCCGGTCTATCGAGAACATCAACGCCCGCTCGCGCGGAGCATCACCG 361
QY 449 ACATCAAGGTCTCCACATCAGTCTCTTCGCGGCTGTCGTGACCTACATATCCCGCTCAG 508
Db 362 GCGTCAGGCGGTCCACGCGGTGAAGTAGACGTCTCACCAACAGCTTCCGCGCGCTCG 421
QY 509 GTGGCTCTCTCTTCGATGATCGTCCGACATCGGTCGAATCGGTCGAATACATACAGTTC 568
Db 422 CCGGCTGTTC-----GGGGCGCTTACATGACGCGCGTGGCCAGCTCTCCGCGAT 472
QY 569 GCAATGGCTCCCCATTTACTTGCACAACTCTACCCCTACTTGGAGCTATGTCGCAATCCG 628
Db 473 GCACCGCGCGCGCTGCTCGCAACATCTACCCCTACTTCCGCTACATCGGCAACAGA 532
QY 629 GATCATCGACTCTCATACGCGCTCTTTACTGATCTGGTACATCTGTACAGGACGGGT 688
Db 533 AGGACATCAGCTCAACTACGCACTTCAGGCGCGGACGACGCTGCGCCGACCAACA 592
QY 689 CCTAC---GCTTACAAACACCTCTTCGATGCCATGCTGCGAGCTATGTCGCGCCCTCG 745
Db 593 CGGACCTGTGTACGCCAACTGTTCGACGCGCATGTCGCTCTACGCGCGCGCTGG 652
QY 746 AGAGCGCGGAGGCGGAAATGTCCCTGTGTGTCGTCGAGAGTGGCTGGCGCTCAGCGG 805
Db 653 ACAAGCGCGCGCGCGCGCTGACGATCGTCTCGGAGAGCGGCTGGCGCTCGCGCG 712
QY 806 CGGAGACAGCGCGGACGCTGTCTAATGCGCAGACTTAACTTCAATTTGATCAACCATG 865
Db 713 GCGGGGACTCGGCGCACGATCGACATCGCGCGGACCTACGTGCGAGAACCTGATTAGCATG 772
QY 866 TGGGTTCAGGGGACCGCGAGAGGCGGCGGAGTTCGAGACCTACATATTTGCCATGTCA 925
Db 773 CGAAGAGGGGACCGCGAA---GCCGGGGGTGATGAGACGTACGTGTTCGCGCATGTCA 829
QY 926 ACAGGATCAGAGCAGCGCGCAAGGATTCGAGAACTTTGGGCTGTTTACCCCTAACG 985
Db 830 ACAGAGACCAAGCGCGGGAAGCCAGGAGCAAACTTTGGAGCCTTCTACCCCTACA 889
QY 986 AACAGCTGTCTATTTCGATCAGCTTC 1011
Db 890 AGACAGCAGTCTACCTATCAATTC 915

RESULT 13

US-09-105-390-53
; Sequence 53, Application US/09105390
; Patent No. 6288303

GENERAL INFORMATION:

; APPLICANT: Rodriguez, Raymond

; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dehlinger & Associates

; STREET: 350 Cambridge Ave., Suite 250

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 996 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...996
; OTHER INFORMATION:
US-09-105-390-53

Query Match 26.2%; Score 295.2; DB 3; Length 996;
Best Local Similarity 59.2%; Pred. No. 9.6e-75;
Matches 586; Conservative 0; Mismatches 383; Indels 21; Gaps 4;

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DB 25 TCTATGTTAAATTTGCTCTGATCATTTGGAGATTGTTCTTGTCTCAACAACTGTGAA 84

QY 85 TCCATTGGGGTCTGCAATGGAATGACGGTGCACAACTCCCGCAGCCGCGCAGTCTGC 144
DB 85 TCCATCGCGGTGTGATGGGTTCTCGGCAACAACTCCCGTGGGAGCGAGTGTG 144

QY 145 AACTCTTAAAGTCAACAAACATAGTGGCATGCGACTTACAGCCCGCAGCAAGCCACT 204
DB 145 CAGCTGTACAAGTCCAAAGGCGATCAACGGCATGGCATCTACTACCCCGACAGAGGCG 204

QY 205 CTCAGGCGCTCCAGGGTCTTAACATCTACCTCATCTCTCGAGTCCCACTCCGACCTC 264
DB 205 CTCACGCGCTCGCAACTCCGGTATCGCCCTCATCTCGAGCTGGCGGACAGTTGTCC 264

QY 265 CAAACATGCTCCGACCAATCCGCGCCCAACCACTGGGTCCAAACCAAGTCCAAAGCC 324
DB 265 AACCTCGCGCGAGTCTCTCCAGCGCGCGGTGGGTCCGGGACAAAGTCAAGGCCCTAC 324

QY 325 TACCCAAACGTTGCTTCGATACATCGCGGTGGGAAAGCAAGTCAATCCCGCGGGCCAA 384
DB 325 TACCGCGCGTCAACATCAAGTACATCGCGGTGGGAAAGCAAGTCAATCCCGCGGGCC 381

QY 385 GCTCAGTACGCTCCCGGCAATGACATACAGTCCGCGCTCTCTCTCGCGGCTT 444
DB 382 ACGAGTACGCTCCCGGCAATGACATACAGTCCGCGCTCTCTCTCGCGGCTT 441

QY 445 CAGAACATCAAGGTCTCACATCAGTCTCTTGGCGGTCTCGGTACCTCATATCCCGCC 504
DB 442 GGGCGCATCAAGGCTTCCAGCGGTGAAGTTCGAGCTCATCTCCAATCTCTACCCACC 501

QY 505 TCAGTGTGCTCTTCTTCGATGCAATGCTGCAATTTGGTTCATATCAAGTTTCTA 564
DB 502 TCGCGCGGTCTTCAGGAGCGCTTACATGAAGGACATCGCGGTCTACCGA----- 552

QY 565 GCCAGCATGCTCCCACTTACTTCCGCAACATCTACCCCTACTTGGATATGCTGGCAAC 624
DB 553 ---TGACCGCGCGCGCTGCTCGCAACAGTGTACCGGTACTTTCGCTTACAGGGGAAAC 609

QY 625 TCCGATCCATGACCTCTCATACGCCCTCTTTTACTGTCATCTGGTACAGT---CGTACAG 681
DB 610 CGCGCGACATCAGCTCTCAATACGCCAGTTCGCGCGGGGACCAACAGTGGAGGCCA 669
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QY 682 GACGGTCTACGCTTACAAACCTCTTGATGCCATGTCGACGCAATGTCATCTCGGCC 741
DB 670 AACACGGGTCTACCTACACCACTGTTCGACCCCATGATGGACGCGGTATCGCCGG 729
QY 742 CTGGAGAGCGCGGAGGGCGGAATGTCCCTTGTTCGTCTCGAGAGTGGCTGGCCGTCA 801
DB 730 CTGGAGAGCGCGGCGCGGGAAGCTGAGGGTGTGTGTCGGAGAGGGGTGGCCGTG 789
QY 802 GCGGGCGGACAGCGGCGAGCGTCTTAATGCGCAGACTTACAATTCCAATTTGATCAAC 861
DB 790 GCGGAGGGTTCGGGGCGAGCGTGCACAATGCGAGGGCGTACAACACGAGGGCTGATCGAC 849
QY 862 CATGTGGTCAAGGGAGCGCGAGAGAGCGGCGGATTCGAGACTACATATTGGCCATG 921
DB 850 CATGTGGT---GGCAGCGCCAGAGCGGCGGCACTGGAGGCGTACATATTGCCCATG 906
QY 922 TTCAACGAGGATCAGAAGCAGCGCCGAGAGCGGCGGATTCAGAAATTAACCTTTGGGCTGTTTACCCT 981
DB 907 TTCAATGAGAACAGAGAGAGCGGGATCCCAACGAGAGAACTTTGGGCTCTTCTACCT 966
QY 982 AACGAACAGCTGTCTATTTCGATCAGCTTC 1011
DB 967 AACAAAGTCCGCGGTATCCCATCCGGTTC 996
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RESULT 14
US-09-105-390-3
; Sequence 3, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
; TITLE OF INVENTION: and Genes
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,390
; FILING DATE: Filed herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,675
; FILING DATE: 25-JUN-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Pettithory, Joanne R.
; REGISTRATION NUMBER: P42,995
; REFERENCE/DOCKET NUMBER: 2000-0455.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-105-390-3
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Query Match 25.5%; Score 286.8; DB 3; Length 2317;
Best Local Similarity 59.8%; Pred. No. 4e-72;
Matches 562; Conservative 0; Mismatches 357; Indels 21; Gaps 4;
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135 CGAGCTGCTCAACCTCTAAGTCCAAAGATAGTGTGCTGAGTCTTACAGCCCGA 194
1453 CGAGGTGGTCAAGCTGTACAGTCCAAAGGCTCAACGCGATCGCGATCTACTACCCGA 1512
195 CCAAGCCACTCTCCAGGCTCCAGGGCTTAACATCTACCTCATCTCGAGTCCCA 254
1513 CAAGAGGGCTCAACGCCCTCGGCACTTCGGTATCGCCCTCATCTCGAGTGGCGA 1572
255 CTCGAGCTCCAAACATTTGCTTCGAGCAATCCGCGCACCAATGGGTCCAAACCAA 314
1573 CCAAGTTGTCAACCTCGCGCGAGCTCTCCAAAGCGCGCGGTGGTCCGCGACAGT 1632
315 GGTCAAGCTACCCAAAGTTGCTTCGATACATCGCGGTGCGAAGAGTATCC 374
1633 CAGGGCTTACTACCGCGCGCTCAACATCAAGTACATCGCGGTGCGCAACAGG--TGA 1689
375 CGCGCGCAAGCTCAGTACGTCTCCAGCCATGAACACATACAGTCCGCCCTCTCTC 434
1690 AGCGCGCGCAGTAGATCTCCGCGCATCGCAAGTCACTCCGCCCTGGGCTC 1749
435 TCGCGGCTTCAGAACATCAAGTCTCCATCAGTCTCTTCGGCGGTGCTCGGTACCTC 494
1750 GGTGCGCTTCGGCGCATCAAGCGCTCCACCGCGGTGAAGTTCGAGCTCATCTCCAACTC 1809
495 ATATCCCGCTCAGTGGCTCTCTCTTCGATGATGCTGCAATTTGGGTCCAATCAT 554
1810 CTACACCGCTTCGGCGCGGTCTTCAGGAGCGCTTACATGAAGGACATCGCGGTACCG 1869
555 ACAGTTTCTAGCCAGCAATGGCTCCCATTTCTGCGCAACATCTACCTTACTTGA 614
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675 ---CTACAGGAGCGGTCTTACGTTTACAAACCTCTTCGATGCGATGGTGGAGCAT 731
1978 GAGGAGCCAAACAAAGCGGTCTCACCTACACCAACCTGTTTCGAGCGCATGATGGAGCGGT 2037
732 GTACTCGGCTTGGAGCGCGGAGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791
2038 GTACCGCGCTTGGAGAGCGCGCGCGCGCGGAAAGTGAAGGTGGTGGTGGTGGAGCGG 2097
792 CTGGCGCTCAGCGCGCGGAGAGCGCGGAGCGGTGTCTAATGCGGAGACTTACAAATCCAA 851
2098 GTGGCGCTTGGGAGAGGTTCGGGCGAGCGGTGAGCAATGCGAGGCGGTACACAGGG 2157
852 TTTGATCAACCATGTGGTTCAGGGGAGCGCGGAGAGCGCGGCGGATTTGAGACCTCAT 911
2158 GCTGATCAGCATGTGCT---GGCAGCGCCAAAGAGCGCGGCGGCGGCGGAGGTATCAT 2214
912 ATTTCATGTTCAAGAGGATCAGAGCGCGGAGCGGATTTGAGATTAATTTGGGCT 971
2215 ATTCCCATGTTCAATGAGAACCAAGAAAGAGGAGTCCCAAGAGAGAAATTTGGGCT 2274
972 GTTTTACCTTAACGAACGCTGCTATTTCGATCAGCTTC 1011
2275 CTTTACCTTAACAGTCCCGGTGTATCCATCCGCTTC 2314

RESULT 15

US-09-105-390-37
; Sequence 37, Application US/09105390
; Patent No. 6288303
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Raymond
; TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..909
OTHER INFORMATION:
US-09-105-390-37

Query Match 24.8%; Score 278.6; DB 3; Length 909;
Best Local Similarity 59.5%; Pred. No. 5.6e-70;
Matches 552; Conservative 0; Mismatches 354; Indels 21; Gaps 4;

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Qy 148 CTCTACAGTCCAAACACATAGCTGGGATGCGATCTTACAGCCCGGACCAAGCCACTCTC 207
Db 61 CTGTACAGTCCAAAGGGCATCAACGGCATGCGCATCTACTACCCCGACAAGAGCGGCTC 120
Qy 208 CAGGCCCTCCAGGCTCTTAACATCTACCTCATCTCCAGCTCCCAACTCCGACCTCCAA 267
Db 121 AACGCCCTTCGCACTCGGTATCGCCTCATCTCGAGCTCGGGACCAAGTTGTCTCAAC 180
Qy 268 AACATTGCTTCGACCAATTCGCGCGCACCAACTGGGTCCAAACCAAGCTCCAGCTTAC 327
Db 181 CTCGCGCGCAGCTCTCTCCAGCGCGCGGTGGGTCCGCGACCAAGTCAAGGCCCTTACTAC 240
Qy 328 CCAAAAGTTCGCTTCGATATACATCGCGGTGGAAACGAGTATCCCCGGGCGGCAAGCT 387
Db 241 CCGCGCGTCAACATCAAGTATACATCGCGTCCGCAACGAGG---TGAAGGCGGCGCCACG 297
Qy 388 CAGTACGTCTCCAGGATGAACAAACATACAGTCCGCGCTCTCTCTGCGCGGCTTCAG 447
Db 298 AGTAGCATCTCCCGGCGCATCCGCAAGTCACTTCGCGCTGGGCTCGGTTCGGCTTCGG 357
Qy 448 AACATCAAGGTCTCCACATCAGTCTCTTCGCGCGTTCGCTGAGTATCTATATCCCCCTCA 507
Db 358 CGCATCAAGGCGTCCACCGGCGTGAAGTTGAGCGTCTATCTCCAACTCTCTCCACCCCTCC 417

GenCore version 5.1.7
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Perfect score: 1125
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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- 10: /cgm2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	431.4	38.3	1333	7	US-10-437-963-64217
3	427.2	38.0	1439	8	US-10-739-930-5127
4	415.6	36.9	3559	3	US-09-892-635A-17
5	394.2	35.0	1458	8	US-10-739-930-5007
6	392.6	34.9	1633	7	US-10-767-701-14878
7	384.8	34.2	1410	8	US-10-425-115-67183
8	381.6	33.9	1268	7	US-10-425-114-26408
9	365.4	32.6	1014	7	US-10-437-963-16329
10	355.4	31.6	1898	7	US-10-437-963-97429
c 11	354.2	31.5	1110	6	US-10-259-165-439
c 12	353.8	31.4	1113	6	US-10-259-165-105
13	348.8	31.0	1464	7	US-10-425-114-20801
14	348.8	31.0	1464	8	US-10-425-115-70439
15	346.2	30.8	1235	3	US-09-138-873A-11
16	343.4	30.5	1235	7	US-10-437-963-34587
17	337.2	30.0	1092	7	US-10-437-963-68666
18	336.2	29.9	1269	7	US-10-767-701-14313
19	334.8	29.8	972	6	US-10-259-165-321
20	334.4	29.7	1296	7	US-10-437-963-8819
21	334.4	29.7	1338	7	US-10-437-963-8823
22	334.2	29.7	4949	7	US-10-437-963-50966
23	332.8	29.6	1188	7	US-10-437-963-8816

†

ALIGNMENTS

RESULT 1

US-10-647-649-2
; Sequence 2, Application US/10647649
; Publication No. US20050048638A1
; GENERAL INFORMATION:
; APPLICANT: individual
; APPLICANT: Chin, Chao-Ying
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID ENCODING BETA-1,3-GLUCANASE FROM LILY
; FILE REFERENCE: 1758-000001/US
; CURRENT APPLICATION NUMBER: US/10/647,649
; CURRENT FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Lily
US-10-647-649-2

Query Match 100.0%; Score 1125; DB 9; Length 1125;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	TTTCATGGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCTGTAGTACTC	60
Qy	61	TCGGCAATCCCGAGAGCGGTGGAATCCATTTGGGGTCTGCAATGGAATGGAACGCTGCAAC	120
Db	61	TCGGCAATCCCGAGAGCGGTGGAATCCATTTGGGGTCTGCAATGGAATGGAACGCTGCAAC	120
Qy	121	CTCCCGCAGCCGCGGAGCGTCTGCTCAACTTACAGTCAACCAATAGTGGCATGCGA	180
Db	121	CTCCCGCAGCCGCGGAGCGTCTGCTCAACTTACAGTCAACCAATAGTGGCATGCGA	180
Qy	181	CTCTACAGCCCGGAGCGGAGCTCTCCAGGCTCCAGGCTCTTAACATCTACTCTATC	240
Db	181	CTCTACAGCCCGGAGCGGAGCTCTCCAGGCTCCAGGCTCTTAACATCTACTCTATC	240
Qy	241	CTCCAGCTCCCAACTCCGACCTCCAAACATTTGCTCCGACCAATCCGCGCCACCAAC	300
Db	241	CTCCAGCTCCCAACTCCGACCTCCAAACATTTGCTCCGACCAATCCGCGCCACCAAC	300
Qy	301	TGGGTCCAAACCAACGTCGAAGCTTACCCAAACGTTGCTTTCCGATACATCGCGTCGGA	360
Db	301	TGGGTCCAAACCAACGTCGAAGCTTACCCAAACGTTGCTTTCCGATACATCGCGTCGGA	360

†

```
QY 361 AACGAAGTATCCCGCGGGCCAAAGCTCAGTACGTCCTCCAGCCATGAAACAACATACAG 420
Db 361 AACGAAGTATCCCGCGGGCCAAAGCTCAGTACGTCCTCCAGCCATGAAACAACATACAG 420
QY 421 TCCGCCCTCTCCTCTGCGGGCCCTCAGAACATCAAGAGTCTCCACATCAGTCTCTTCGGC 480
Db 421 TCCGCCCTCTCCTCTGCGGGCCCTCAGAACATCAAGAGTCTCCACATCAGTCTCTTCGGC 480
QY 481 GTCGTGGTACCTCATATCCGCCCTCAGTGGCTCCTCTCTTCGATGATCGTGCACA 540
Db 481 GTCGTGGTACCTCATATCCGCCCTCAGTGGCTCCTCTCTTCGATGATCGTGCACA 540
QY 541 TTGGGTCCCAATCATACAGTTTCTAGCCAGCAATGCTCCCAATTAATTTGCGCAATCTAC 600
Db 541 TTGGGTCCCAATCATACAGTTTCTAGCCAGCAATGCTCCCAATTAATTTGCGCAATCTAC 600
QY 601 CCCTAATTGAGTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACT 660
Db 601 CCCTAATTGAGTATGCTGGCAACTCCGGATCCATCGACCTCTCATACGCCCTCTTTACT 660
QY 661 GCATCTGGTACGTGTAAGAGCGGGTCTTACGGTTTACAAACATCTTTCGATGCCATG 720
Db 661 GCATCTGGTACGTGTAAGAGCGGGTCTTACGGTTTACAAACATCTTTCGATGCCATG 720
QY 721 GTCGACGATTTGCTCGGCCCTGAGAGCGCGGAGCGCGGCGGAGTGTCCCTGTTGCTG 780
Db 721 GTCGACGATTTGCTCGGCCCTGAGAGCGCGGAGCGCGGCGGAGTGTCCCTGTTGCTG 780
QY 781 TCGGAGAGTGGTGGCCGCTCAGCGGGCGGGAGCAGCGGCGAGCGTGTCTAATGCGCAGACT 840
Db 781 TCGGAGAGTGGTGGCCGCTCAGCGGGCGGGAGCAGCGGCGAGCGTGTCTAATGCGCAGACT 840
QY 841 TACAATTCGAATTTGATCAACATGCGGTGAGGGAGCGCGGAGAGCGCGGCGGATTT 900
Db 841 TACAATTCGAATTTGATCAACATGCGGTGAGGGAGCGCGGAGAGCGCGGCGGATTT 900
QY 901 GAGACCTACATTTGGCCATGTTCAACGAGGATCAGAGCGCGGCGGAGGATTTGAGAA 960
Db 901 GAGACCTACATTTGGCCATGTTCAACGAGGATCAGAGCGCGGCGGAGGATTTGAGAA 960
QY 961 AACTTTGGGCTGTTTACCTTAACGAAACAGCGCTGTCTATTGATCAGCTTCACTTGAGAA 1020
Db 961 AACTTTGGGCTGTTTACCTTAACGAAACAGCGCTGTCTATTGATCAGCTTCACTTGAGAA 1020
QY 1021 ATTGATCAGATGAATATAATAAAGTCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
Db 1021 ATTGATCAGATGAATATAATAAAGTCTTATATTGTAAGGCAAGCTCGTAATTGA 1080
QY 1081 TAGCCATCTAGTAATATAGCTCCGCTTAATTAATACTATAAATA 1125
Db 1081 TAGCCATCTAGTAATATAGCTCCGCTTAATTAATACTATAAATA 1125
```

RESULT 2

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US-10-437-963-64217
; Sequence 64217, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
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; SEQ ID NO 64217
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65383C.1
US-10-437-963-64217
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Query Match 38.3%; Score 431.4; DB 7; Length 1333;
Best Local Similarity 66.8%; Pred. No. 3.8e-124;
Matches 682; Conservative 0; Mismatches 321; Indels 18; Gaps 4;
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QY 4 ATGCAGCTCAGCACATCATCTCCATGGCTGCCATGGCATCCCTCCTGTGTAGTACTCTCG 63
Db 112 ATGCAAAAGCATGGGTGCTTCCGTTTAACATGGCATGGTGGTCTTGGAG---TTGGG 168
QY 64 GCAATCCCGAGAGCGGTGGAATCCATTGGGTCTGCAATGGAATGGACGGTGAACAACCTC 123
Db 169 GCCATTCTACAGTGGTGCATCTATCGGCGTGTGTACGGCGTGTATCGGCGTGTATCGGAAACAACCTG 228
QY 124 CCCAGAGCCGCGAGCGTGTCAACCTCTACAGTCCCAACACATAGCTGGCATGGACTC 183
Db 229 CCGTCGCGAGCGAGCTGTGTCAGCTCTTACAAGTCCCAACGGCATCGATCTCATGCGCATC 288
QY 184 TACAGCCCGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAACATCTACTCTCATCTC 243
Db 289 TACTTCCCAAGAAGCGACATCTCTCAGGCCCTCAGCGGCTCAAGCATGCCCTCACCATG 348
QY 244 GACGTCCCAACTCCGACCTCCAAAATGTCCTCCGACCAATCCGCGGCGCACCAACTGG 303
Db 349 GACGTCCGCAACGATCAGTCCGCTCTCCGCTCCGACCCCTCCGCGCGCGCGCTTC 408
QY 304 GTCCAAACCAACGTCGAGCCTACCCAAAGTTCGCTTCGATACATCCGCTCGGAAC 363
Db 409 GTCCAGAAACAATCCAGGGCTTCCCGGGCGTCAACTTCGCTACATCACGGTCGGCAAC 468
QY 364 GAAGTCATCCCGCGCGGCAAGCTCAGTACGCTCTCCAGGCATGAAACAATACAGTCC 423
Db 469 GAGG---TTTCCGGCGGGACACGCGAACAATCTCCGGCCATGCGAACAATGNAACAGC 525
QY 424 GCCCTCTCTCTGCGGCTTTCAGAACATCAAGGTCTCCACATCAGTCTCTTTCGGGCTC 483
Db 526 GCCCTCTCCGCGCGGCTTCGGCAACATCAAGGTGTGACGTCGGTGTCTCCAGGGCTG 585
QY 484 GTCGTACTCATATCCCCCTCAGCTGGCTCTCTCTTCCGATGCACTCGTCGACATG 543
Db 586 ACCG---CCGGCTTCCGCGCGTCCGCGGCACTTCTCCGCT---TCGCACATG 633
QY 544 GGTCCAAATCATACAGTTTCTAGCCAGCAATGGCTCCCAATTAATTTGCCAATCTTACCCC 603
Db 634 GGGCCCATAGCTCAGTACCTGCGAGCACCGCGCGGCGGCTGTCTGCGCAAGTCTTACCCC 693
QY 604 TACTTGAGCTATGCTGGCAACTCCGGATCCATCGAACCCTCTCATACGCCCTCTTTACTGCA 663
Db 694 TACTTGGCTTACGTGGGCAACAGCGCCAGATCGACATCAACTACGCGCTCTTTCACGTCG 753
QY 664 TCTGTACAGTCGTACAGGAGGGTCTTACGTTTACACACACCTTTCGATGCCATGCTC 723
Db 754 CCGGCGACGGTGGTGCAGGACCGGCGCAACCGTACCAAGAACCTGTTTCAGCGCCATCGTC 813
QY 724 GACGATTTGACTCGGCCCTCGAGAGCGCGCGGCGCAATGTCCCTGTTGTGTGTGTGTCG 783
Db 814 GACAGTTTCTACTCGCGCTGGAGAGCGCGCGCGGCGGAGCGTCCCGATCGTGTGTGTCG 873
QY 784 GAGAGTGGCTGGCGCTCAGCGGGCGGGACAGCGCGGAGCGGTGTCTAATGCGCAGCTTAC 843
Db 874 GAGAGCGGGTGGCGCTCGGCGCGGCGACGCGCGGCGGCGGCGCAACCGCGCAGACGTCAC 933
QY 844 AATTCCAAATTTGATCAACCATGTGGTTCAGGGGAGCGCGAGAGCCAGGGCGGCTTAC 903
Db 934 AACCAGAAACCTGATCAACACGTCGGGCGAGGGGACGCCCAAGAGGCCCGGGGAGCATCGAG 993
QY 904 ACCTACATATTTGCCATGTTCAACAGGATCAGAAGCAGCGCGCAAGGATTTGAGAATAAC 963
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Db 994 ACCACATTTTCGCCATGTTCAACGAGAACCCAGAGGGAGGCGACGAGACGGAGGCAC 1053
Qy 964 TTGGGCTGTTTACCCCTAACGAAACAGCCTGTCTATTTCGATCAGCTTTCACTTTGAGAAAT 1023
Db 1054 TTGGGCTCTTCAACCCGAGCAGCTGCGCGGATCTCCATCAATTTCTAAGAGATTGT 1113
Qy 1024 T 1024
Db 1114 T 1114

RESULT 3
US-10-739-930-5127
; Sequence 5127, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; ; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; PRIORITY FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5127
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1439)
; OTHER INFORMATION: unsure at all n locations
; ;
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTERS79_3
US-10-739-930-5127

Query Match 38.0%; Score 427.2; DB 8; Length 1439;
Best Local Similarity 66.0%; Pred. No. 8.4e-123;
Matches 656; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

Qy 21 CATCTCCATGGTGCATGGCATCCCTCTGTGTAGTACTCTCGGCAATCCCGAGAGGGGT 80
Db 96 CATGTTTTCGGTGGCGTTTGGCCCTTCTTGGAGTGTCTTGGGATCCATTCTCTGACGCGT 155
Qy 81 GGAATCCATTGGGGTCTGCAATGGAATGAGCGGTGACCACTCCCGGAGCGCGCGAGGT 140
Db 156 GCAATCCATCGCGGTGTACTCGGCGTGAACGGCGAGCGCTGCGCTCGGCGAGGAAAT 215
Qy 141 CGTCAACCTCTACAAGTCCAAACATAGCTGGCATGGGACTCTACAGCCCGGACCAAGC 200
Db 216 CGTGAGCTCTACCAAGTCCAAAGGATCACCGGATGCGCATCTACTTCCCGGAGCGGA 275
Qy 201 CACTCTCAGGCGCTTCAGGGCTTAAACATCTACCTCATCTCTGAGCTGCCCACTCCGA 260
Db 276 CGCCCTCAGGCGCTTCAGGCGGAGCAACATCGACCTCATCTGACGCTGGGCAACGAGGA 335
Qy 261 CCTCCAAACATGCTCCGACCAATCCGCGCGCACCACTGGGTCCAAACCAAGTCCA 320
Db 336 CTTCCCTCTCCCTCGCGCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 395
Qy 321 AGCTTACCAACAGTGTGCTTCCGATACATCGCGCTCGGAAACGAAGT---CATCCCGG 377
Db 396 GCGCCACAGGCGCTCAACATCAAGTATCATCGCGCGCGCGCGCGCGCGCGCGCGCGCG 455
Qy 378 CGCGCAAGCTCAGTACGCTCTCCAGCGCATGAAACATACAGTCCGCGCTCTCTCTGCG 437
Db 456 CGCGGACAGGCGGACATCTCCCGCGCATGAGAACTCGAGCGCGCACTCTCCGCGCG 515
Qy 438 CGGCTTCAGAACATCAAGGTCTCCACATCAGTCTCTTCCGCGCTGCTGCTGCTACTATA 497
Db 516 CGGGCTAGCGGCGCATCAAGGTGTCCACGCTCGGTGTGCGAGGCGGTGACCGCGCGCTACC 575
Qy 498 TCCCCCTCAGCTGGCTCTTCTCTTCGATGTCATCGTTCGATGTTGGGTCCAATCATACA 557

Db 576 TCCCTCCCAAGGACACTTCTCCGCGGCTACA-----TGGAGCCCATCGCGCA 623
Qy 558 GTTTCAGCGCAATGGTCCCATTTACTTGGCAACATCTTACCCCTACTTGAAGTATGC 617
Db 624 GTACTGGCGCACCAACCGCGCGCGCTGCTCGCCAAACGTTTACCCCTACTTCTCGTACGT 683
Qy 618 TGGCAACTCCGATCCATCGACCTCTCATACGCGCTCTTTTACTGATCTGGTACAGTCTGT 677
Db 684 GGACAAACAGGCGCCAGATCGACATCACTACGCGCTCTTCACTGCGCGGACCGTGTGT 743
Qy 678 ACAGGACGGGTCTTACGTTTACAAACCTCTTTCGATGCACTGGTTCGAGCGCATTTGACTC 737
Db 744 GCAGGACGGCGCAACGCGGTACCAAGAACTGTTCGACGCGCTCGTCGACACGCTTCTACTC 803
Qy 738 GGCCTCGAGAGCGCGGAGGCGGCAATGTCTCTGCTGCTGCGAGAGTGGCTGGCC 797
Db 804 CGCGCTCGAGAGCGCGGCGCGGCGGAGCGTCAACGTTGGTGTGTCGAGAGCGGGTGGCC 863
Qy 798 GTACGCGCGCGGACAGCGGCGACGCGTGTCTTAATGCGCAGACTTACAAATTTCAATTTGAT 857
Db 864 GTGCGCGCGGCGACGCGGCGGCGACAAACGCAACGCGGAGCGTACAAACGAGACCTCAT 923
Qy 858 CAACCATGTGGTTCAGGGGACCGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 917
Db 924 CAACCATGTGGGCAAGGCGACCGCCCAAGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 983
Qy 918 CATGTTCAACGAGATCAGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 977
Db 984 CATGTTCAACGAGGACAAAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1043
Qy 978 CCCTAACGAACAGCGCTGTCTATTTCGATCAGCTTC 1011
Db 1044 CCGGACAAATCGCGCGGTACCCCATCAGTTTC 1077

RESULT 4

US-09-892-635A-17
; Sequence 17, Application US/09892635A
; Publication No. US20030226175A1
; GENERAL INFORMATION:
; APPLICANT: May, Gregory D.
; APPLICANT: Clendennen, Stephanie K.
; APPLICANT: Mason, Hugh S.
; APPLICANT: Lim, Miguel A. Gomez
; APPLICANT: Artzen, Charles J.
; TITLE OF INVENTION: DNA Regulatory Elements Associated with Fruit Development
; FILE REFERENCE: 031998-007
; CURRENT APPLICATION NUMBER: US/09/892,635A
; PRIORITY FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/160,351
; PRIORITY FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: US 60/060,062
; PRIORITY FILING DATE: 1997-09-25
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 3559
; TYPE: DNA
; ORGANISM: Musa acuminata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3559)
; OTHER INFORMATION: Complement
US-09-892-635A-17

Query Match 36.9%; Score 415.6; DB 3; Length 3559;
Best Local Similarity 68.2%; Pred. No. 6e-119;
Matches 670; Conservative 0; Mismatches 294; Indels 18; Gaps 6;

Qy 75 AGGCGTGAATCCATTTGGGTCTGCAATGGAATGAGCGGTGCAACACCTTCCCGGAGCGCGC 134
Db 2078 AGGAGTCAATCGATTGGTGTCTGCTACGGAATGCTCGGCAACATCTTTCGCGCGCCAG 2137

QY 915 TGGCAAGTTCAACGAGGATCAGAGCGCGGCAAGGGATTGAGATAAATTTGGGCTGTT 974
Db 945 CTCCTATGTTCAACGAGAACCAAGAGGA---CAGCGCGGTGGAGCAGAACTGGGGAATCTT 1001
QY 975 TTACCCTTAACGAGACGCTGCTTATTCGATCAGCTTCACTTCAGAAATTTG 1025
Db 1002 CTACCCCAACATGACACGCTTACCCCATCAGCTTCTGATGAGCTAGCTG 1052

RESULT 6

US-10-767-701-14878
; Sequence 14878, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 14878
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3480_1
US-10-767-701-14878

Query Match 34.9%; Score 392.6; DB 7; Length 1633;
Best Local Similarity 63.2%; Pred. No. 6.7e-112;
Matches 643; Conservative 0; Mismatches 359; Indels 15; Gaps 2;

QY 4 ATGGCAGCTCAGCACATCATCTCCATGGCTGCATGGCATGCGATCCCTCTTGTAGTACTCTCG 63
Db 107 ATGGCGAGGACGATGATCGTCTCCATGCTTGCATCTGCACTGGCATTTCTCTCGGAGCAATTGCA 166
QY 64 GCAATCCGAGAGGGGTGGAATCCATTTGGGTCTGCAATGGAATGAGCGGTGACAACTC 123
Db 167 GCATCTCTACGAGAGTCAAGCCATCGGGGTGTCTAGCGGTGAACGGGACAACTG 226
QY 124 CCCAGCCGCGCAGCTCGTCAACCTCTACAGTCCAAACAAATAGCTGGCATGCGATC 183
Db 227 CGTGGCGAGCGAGCTGTGAACTGTACAGTCCAAAGGATCACTGATGCGCATC 286
QY 184 TACAGCCCGACCAAGCACTCTCAGGCCCTTCAGGGCTTCAAGCTTCACTCATCTC 243
Db 287 TACTTCGGGACACCAACGCGCTCAACGCGCTGAGCGGCGCAACATCGGGGTGATCATG 346
QY 244 GAGCTCCCAACTCCGACCTCCAAACATTCCTCCGACCAATCGCGCGCCACCACTGG 303
Db 347 GAGTGGCCCAACAGGACCTCTCTCGCTGGCTCCGACCCGAGCGCGGCGGCGACGTTG 406
QY 304 GTCCAAACCAAGCTCAAGCTTACCAACAGTTGCTTCCGATACATCGCGCTCGGAAC 363
Db 407 GTGAAGACCAAGCTGACAGCGTTCCCGGGGTCACTTCAAGTACATCGCGCTCGGCAAC 466
QY 364 GAAGTATCCCGGGCGCAAGCTCAAGTCAAGTCTTCCAGCGCATGAACAAATACAGTCC 423
Db 467 GAGG---TCTCGGGGGGACACCAACCAATCTCTCCCGCCATGAAGAACTCAACTCG 523
QY 424 GCGCTCTCTCTCGCGGCTTCAGAACATCAAGTCTCCATCATCATCTCTCTCTCGGCTC 483
Db 524 GCGTGTCCAAAGCGGGGTGGGAAGATCAAGGTGTCCAGCGGGGTGACAGAGCGGCTC 583
QY 484 GTCGTACTCATATATCCCGCTTCAGCTGGCTCTCTCTCTCGGATGATCGTCGACATTG 543
Db 584 ACGAGGGGTACCGCGCTGCGAGGGGAGCTTCTCGAGAGGTAC-----ATG 631
QY 544 GGTCAATATACAGTTTCTAGCCAGCAATGGCTCCCATTAATCTTGGCAATCTACCCC 603

Db 632 GCGCCCATCGCGCAGTACTCTGACAGACACGCGGGGCGCCGCTCTCTCTGCAACGCTCTACCCC 691
QY 604 TACTTGGAGTATGCTGGCAACTCCGATCCATCGACCTCTCATACGCGCTCTTTACTGCA 663
Db 692 TACTTCTCTACACGGGCAACGAGGCCAGATCGCCCTCAGCTACGCGCTCTTCAAGCTG 751
QY 664 TCTGTCACAGCTGTACAGGACGGGTCTTACGCTTACAAACAACTCTTGGATGCCATGGTC 723
Db 752 CGGGGACCGTCTGTCAGGACGGCAGCAACGGTACCAGAACCTCTTCGACGGGCTCGTC 811
QY 724 GACGATTTGTTACTCGGCCCTGAGAGCGCGGAGGGCCGAATGTCCCTGTTGTCGTCG 783
Db 812 GACACTTTCGTTCGCGCTCGAGAAACGCGCGCGCGGGAACGTCGGGCTCTGCTGTGTC 871
QY 784 GAGAGTGTGCGCGCTCAGCGGGGACAGCGGCGAGCGGTCTCTAATGCGCAGACTTAC 843
Db 872 GAGAGCGCTGTGCGCTCGCGCGCGGAGCGCGCCAGCGCGGGAACGCGCAGACCTTAC 931
QY 844 AATTCCAATTTGATCAACCATGTGGTTCAGGGGACGCGGAAGAGCGCCAGGGCGGATGAG 903
Db 932 AACCAAGACCTCATCAACCATGTGCGGGAAGGCGACGCCCAAGCGGCCCGCCATCGAG 991
QY 904 ACCTACATATTTGCCATGTTCAACGAGGATCAGAGCAGCGCGCAAGGAGGATGAGAAATAC 963
Db 992 ACCTACATCTTTCGCCATGTTCAACGAGGACAAAGAGACGCGGAGCGGAGGAGGCAC 1051
QY 964 TTTGGGCTGTTTATACCTTAACGACAGCGCTCTTATTCGATCAGCTTCACTTGAGAA 1020
Db 1052 TTGGAGCTCTTCAACCCCGGACAAATCGCGCGGCTACTCCATCAATTTCTCTCTTAAAAA 1108

RESULT 7

US-10-425-115-67183
; Sequence 67183, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 67183
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_161268C.1
US-10-425-115-67183

Query Match 34.2%; Score 384.8; DB 8; Length 1410;
Best Local Similarity 63.1%; Pred. No. 1.7e-109;
Matches 631; Conservative 0; Mismatches 357; Indels 12; Gaps 2;

QY 18 CATCATCTCCATGGCTGCCATGGCATCCCTCTTGTAGTACTCTCGGCAATCCGAGAGG 77
Db 187 CGTGGTTCATGATGATGCGTGGCATTTGCTTCTCGAGCATTCGAGGCAATTCCTACAGG 246
QY 78 CGTGGATCCATTTGGGTCTGCATGGAATGAGCGGTGACAACTCCCGCCAGCCGCGCA 137
Db 247 AGTCCAAATCCATCGCGGTGTGCTACGCGGTGAACGCGGACAACTGCGCGGAGGCA 306
QY 138 CGTGTCAACCTCTFACAAAGTCCAAACATAGCTGGCATCGAGCTCTTACAGCCCGGACCA 197
Db 307 CGTGTGAGGTGTACAGGTCCAAAGGATCAACCTGATGCGCATCTACTTCCGAGCGC 366
QY 198 AGCCACTCTCAGGCCCTCCAGGGCTCTAAACATCTACCTCATCTCAGAGTCCCAACTC 257
Db 367 GAAAGCTGAACGCGCTGAGCGGCAACGAGCATCGGGCTCATCATGAGAGTGGCCCAACAC 426


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Db 334 CGCCGCGGAGCTCGTGGTGGGATGTACCGCTCAAGGGATCACGTGCATGCGGGTG 393
Qy 184 TACAGGCGGAGCAAGACCACTCTCAGAGCCCTTCAAGGCTCTTAACATCTACTCATCTC 243
Db 394 TACGCGCGGACACAGCGCGCTGCACTCGGTGGGCGGACAGGGGATCAGCGTCTGCTC 453
Qy 244 GAGCTCCCAACTCCGACTCCAAACATTTGCTTCGAGCAATCGCCGCGCACCACTGG 303
Db 454 GCGCGCGCAACAGAGCTCTTCCAACTCGCGCGCACGCCCGCGCGCGCGCTGCTGG 513
Qy 304 GTCCAAACCAACGCTCAAGAGCTTACCCAAAGTGTGCTTCCGATACATCGCGCTCGAAAC 363
Db 514 GTGCGGAACACATCCAGGCTTACCGCTCGGTGTGCTTCGGTACGTGCGCGTGGAAAC 573
Qy 364 GAAGTCACTCCCGCGGCAAGCTCAGTACGTCTCCAGGCAATGAACAAATACAGTCC 423
Db 574 GAGG---TCGCGCGGCGGCCACGCTCCAGCTGGTTCGCGGCATGGAGAACGTTCGGGGC 630
Qy 424 GCCCTCTCTCTGCGCGGCTTCAGAACATCAGGTCTCCATCAGTCTCTTTCGGCGTC 483
Db 631 GCGCTGGTGTGGCGGGGCTGGGGCCACATCAAGGTGACGAGCTCTCTTACGCGCTC 690
Qy 484 CTCGTACTCTCATATCCCCCTCAGTGGCTCTTCTTCCGATGATCGTGCACATTTG 543
Db 691 CTCGCGGTGTACAGCCCGCGCTCCGCGGGAGTTACCGGGAGTCGCGAGGCTTCATG 750
Qy 544 GGTCAATCATACAGTTTCTAGCAGCAATGGCTCCCAATTAATCTTTCGCAACATCTACCC 603
Db 751 GCGCCCGCTCTGAGCTTCTCGCGCGCACCGCGCGGCTGCTCGCCCAACATCTACCC 810
Qy 604 TACTTGACTATGTGGCAATCCGGATCCATCGACTCTCATAGCCCTCTTACTGCA 663
Db 811 TACTTCTCTACCTACAGCCAGGGCAGCGTGCAGAGCTCTCTTACGCGCTCTTACCGCC 870
Qy 664 TCTGTACAGTCTGACAGAGGGTCTTACGCTTACAAACACCTCTTCGATGCGCATGTC 723
Db 871 GCGCGCACGCTGTCTAGAGACGGCGCTTACGGGTACAGAACCTGTTCGACACACCGTC 930
Qy 724 GACGATTTGTAATCGGCTCTGAGAGCGCGGAGCGGCGGATGTCCCTGTTGTGCTGTCG 783
Db 931 GACGCTTTCTACGCGCGCATGCCAAGCACGCGGCTCCGCGCTCTCCTCGTCTCTCC 990
Qy 784 GAGATGCTGGCTGACGCGGCGGAGACGGGCGAGCGTGTCTAATGCGGACTTAC 843
Db 991 GAGACCGGCTGGCCCTTCGCGCGGGGCAATGTCCGCTCGCGCGCAACGCGCGGATCTAC 1050
Qy 844 AATTCCAATTGATCAACATGTGGGTGAGGGAGCGCGAAGAGCGGAGGGCGGATTCAG 903
Db 1051 AACCGAACCTCATCNACACAGTGGCGCGGCGACGCGCGGCAACCGCGGCGCATCGAG 1110
Qy 904 ACCTACATATTGGCATGTTCAAGAGATCAGAGAGCGCGCAAGGGAATGAGAAATAC 963
Db 1111 ACCTACGCTTCTTCCATGTTCAACAGAAACAGAGAGGAGCGC---CGGGGTGAGCAGAT 1167
Qy 964 TTTGGCTGTTTACCTTAACGACAGCTGTCTATTGATCAGTTTCACTTG 1016
Db 1168 TGGGGCTCTTCTTACCCCAACATGACGACAGCTCTACCCCATCAGGTTCTGATG 1220
```

RESULT 11

US-10-259-165-439/c

; Sequence 439, Application US/10259165
; Publication No. US2003013988A1

GENERAL INFORMATION:

; APPLICANT: Zhu, Tong

; APPLICANT: Wang, Xun

; APPLICANT: Chang, Hur-song

; APPLICANT: Briggs, Steven P.

; APPLICANT: Cooper, Bret

; APPLICANT: Glazebrook, Jane

; APPLICANT: Goff, Stephen A.

; APPLICANT: Katagiri, Pumiaki

; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (c) 2001 Syngenta
; SEQ ID NO 439
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-439

Query Match 31.5%; Score 354.2; DB 6; Length 1110;

Best Local Similarity 60.9%; Pred. No. 6.3e-100;

Matches 613; Conservative 0; Mismatches 388; Indels 6; Gaps 2;

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Qy 244 GAGTCTCCCACTCGGACCTCCAAACATTTGCTCTCCGCAATCGCGCGGCGGCGTGTGG 303
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Qy 789 TGGTGGCGCTCAGCGGCGGAGACGCGGAGCGGCTGTCTAATGCGCAGACTTACATTC 848
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RESULT 15

US-09-138-873A-11

; Sequence 11, Application US/09138873A

; Publication No. US20010020300A1

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Transgenic pathogen-resistant organism

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Baker & Botts

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/138,873A

; FILING DATE: August 24, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Tenser, Arthur

; REGISTRATION NUMBER: 18,839

; NAME: Kole, Lisa

; REGISTRATION NUMBER: 35,225

; REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 408-2500

; TELEFAX: (212) 765-2519

; TELEX: 238555

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1235 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Hordeum vulgare

; STRAIN: L.

; FEATURE:

; NAME/KEY: 5'UTR

; LOCATION: 1..48

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 49..1050

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OTHER INFORMATION: /product= "preprotein of the glucanase GluG"
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LOCATION: 1051..1235
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FEATURE:
NAME/KEY: polyA_signal
LOCATION: 1083..1088
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NAME/KEY: polyA_signal
LOCATION: 1210..1215
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NAME/KEY: mat_peptide
LOCATION: 133..1050
US-09-138-873A-11

Query Match

30.8%; Score 346.2; DB 3; Length 1235;

Best Local Similarity 60.4%; Pred. No. 2.2e-97;

Matches 611; Conservative 0; Mismatches 388; Indels 12; Gaps 2;

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Db 49 ATGGCTAGAAAGATGTTGCTTCCATGTTTGAGTTGCTCTTTCATTGGAGCATTCGT 108
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Qy 184 TACAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Db 229 TACTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
Qy 244 GACGTCCCGCAACTCCGAGCTCCAAACATTTGCTCCGCAACATCCGCGCGGAGGAGGAGGAGGAG 303
Db 289 GACATGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
Qy 304 GTCCAAACCAACGCTCAAGGCTTACCCAAAGGCTTTCGATACATCGCGGTGCGAAAC 363
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Qy 364 GAAGTCATCCCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
Db 409 AACGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
Qy 424 GCGCTCTCTCTGCGCGCTTTCAGAAACATCAAGGTCTCCACATCAGTCTCTTTCGGCGTC 483
Db 469 GCGCTCTCTGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 528
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QY 820 TCGGAGAGCGGTGGCCGCTCGGCGGCGGGTTTGGCGGTGCGCGGCAATGCGCGGACG 879
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QY 880 TACAACCAAGGGGCTGATCAACCATGTGCGCGGGGCGACGCCGAGAGGGGAGGCGCTG 939
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Job time : 1109 secs

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OM nucleic - nucleic search, using sw model

Run on: April 7, 2006, 20:54:59 ; Search time 661 Seconds
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Title: US-10-647-649-2

Perfect score: 1125

Sequence: 1 ttcatgcagctcagcacat.....ctaataaaactataaata 1125

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA_New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	86.2	7.7	491	11	US-11-116-881A-2189
3	86.2	7.7	546	11	US-11-116-881A-1704
4	80.8	7.2	386	11	US-11-116-881A-703
5	76.6	6.8	487	11	US-11-116-881A-1232
6	55.6	4.9	1330	11	US-11-096-568A-9277
7	54.8	4.9	9903	14	US-11-052-554A-517
8	49.6	4.4	1501	14	US-11-138-987-16
9	48.2	4.3	6645	14	US-11-128-061-426
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13	47.2	4.2	88421	14	US-11-205-109-1
14	47	4.2	142303	14	US-11-121-086-42
15	47	4.2	165911	11	US-11-114-798-52
16	46.8	4.2	2304	14	US-11-052-554A-538
17	46.8	4.2	6210	14	US-11-056-470-1
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19	45.8	4.1	1108	11	US-11-096-568A-11282	Sequence 11282, A
20	45.8	4.1	4983	14	US-11-052-554A-521	Sequence 521, App
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27	43.8	3.9	773	14	US-11-110-082-3	Sequence 3, Appli
28	43.8	3.9	1167	14	US-11-228-659-19	Sequence 19, Appli
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34	43.2	3.8	2135	11	US-11-096-568A-11555	Sequence 11555, A
35	43	3.8	1613	14	US-11-024-959-71	Sequence 71, Appl
36	43	3.8	2562	14	US-11-052-554A-533	Sequence 533, App
37	42.6	3.8	1379	11	US-11-096-568A-16670	Sequence 16670, A
38	42.6	3.8	1741	11	US-11-096-568A-13489	Sequence 13489, A
39	42.6	3.8	57073	8	US-10-995-561-13275	Sequence 13275, A
40	42.2	3.8	4581	9	US-10-932-182A-79437	Sequence 79437, A
41	42.2	3.8	4581	9	US-10-932-182A-79437	Sequence 79437, A
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45	41.8	3.7	1450	11	US-11-096-568A-12512	Sequence 12512, A

ALIGNMENTS

RESULT 1

US-11-116-881A-1842
; Sequence 1842, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1842
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-1842

Query Match 7.7%; Score 86.2; DB 11; Length 438;

Best Local Similarity 53.9%; Pred. No. 2e-14;		Best Local Similarity 53.9%; Pred. No. 2.1e-14;	
Matches 200; Conservative 0; Mismatches 168; Indels 3; Gaps 1;		Matches 200; Conservative 0; Mismatches 168; Indels 3; Gaps 1;	
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Db	194 CAAATCATGGAGCTTTTACAGCATTTAAAGGCTCAAATATTGAAGTTATGTTAGGACTTC 253	Db	220 CAAATCATGGAGCTTTTACAGCATTTAAAGGCTCAAATATTGAAGTTATGTTAGGACTTC 279
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Qy	311 CCAACGTCCAAG---CCTACCCAAACGTTGCTTCCGATACATCCCGCTCGGAACGAAG 367	Qy	311 CCAACGTCCAAG---CCTACCCAAACGTTGCTTCCGATACATCCCGCTCGGAACGAAG 367
Db	314 AAAATGTTAAAGATTTCTGGCCAGATGTTAAGATTAAGTATATTGCTCTTGGGAATGAAA 373	Db	340 AAAATGTTAAAGATTTCTGGCCAGATGTTAAGATTAAGTATATTGCTCTTGGGAATGAAA 399
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RESULT 2

US-11-116-881A-2189
; Sequence 2189, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/646,764
; PRIOR FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: 60/607,357
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/566,235
; PRIOR FILING DATE: 2004-04-29
; PRIOR APPLICATION NUMBER: 10/934,944
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 10/943,507
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2189
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-2189

Query Match 7.7%; Score 86.2; DB 11; Length 491;

RESULT 3

US-11-116-881A-1704
; Sequence 1704, Application US/11116881A
; Publication No. US20060041949A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; APPLICANT: Nielsen, Mark T.
; TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof
; FILE REFERENCE: 07678/141014
; CURRENT APPLICATION NUMBER: US/11/116,881A
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/665,451
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/665,097
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; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/503,989
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; PRIOR APPLICATION NUMBER: 60/485,368
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/418,933
; PRIOR FILING DATE: 2002-10-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2300
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1704
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-11-116-881A-1704

Query Match 7.7%; Score 86.2; DB 11; Length 546;

Db 228 AGATACAAATGCTTCAACGCTCTCAGAGGAAGTAACATTGAGATCATTTCTCGAGTCCC 287
Qy 252 CAATCCGACCTCCAAACATTTGCTCCGACCAATCCGCGGCCCACTGGTCCAAAC 311
Db 288 ACTTCAAGATCTTCAATCCCTAACTGATCTTCAAGAGCCCAATGGATGGTCCAGATAA 347
Qy 312 CAACGCTCAAGCTTACCCAAAGTTGCTTCCGATACATCCGCGCGGAACGAGTCAAT 371
Db 348 CATAATAATCATTTCCAGATGTTAAATTAATATATAGCTGTTGGAATGAAGTCTC 407
Qy 372 CCCCGCGGCCCAAGCTCAGTACG 394
Db 408 TCCCGGAATAATGTCATATG 430

RESULT 6

US-11-096-568A-9277
; Sequence 9277, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9277
; LENGTH: 1330
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1330)
; OTHER INFORMATION: Ceres Seq. ID no. 15179743
US-11-096-568A-9277

Query Match 4.9%; Score 55.6; DB 11; Length 1330;
Best Local Similarity 45.6%; Pred. No. 2e-05;
Matches 196; Conservative 0; Mismatches 234; Indels 0; Gaps 0;
Qy 86 CATTGGGGTGTGCAATGGAATGGAGCGTGACAACTCCCGCAGCGCGCGAGCTGGTCA 145
Db 47 CATTGGCGATCTCCCGCGCTCTCTCTCCCGCTCTCTCTCCCGCGCGCGCGCTCCG 106
Qy 146 ACCTCTACAAGTCCAAACATAGCTGGCATGCGACTCTACAGCCCGCCGACCAAGCCATC 205
Db 107 CTTGCGCGCGCCAAACGACCTGTGTGGGAGCTCCAGTCCCTCGCTCCCGCTCCCGC 166
Qy 206 TCCAGGCCCTCCAGGGCTTAAATCTATCTATCTCGAGTCCCGCAACTCCGACCTCC 265
Db 167 CCGCGGTGATCCACTCAACGACACTCCGTCCGCTCACCCTGCTCTCTCTCGCGCGCGCGC 226
Qy 266 AAACATTTGCTCCGACCAATCCGCGCCGACCACTGGGTCCAAACCAAGCTCCAGGCT 325
Db 227 GCGCCCTACTCGTCTCTGCTTTTCGAGCGCCACCTCGCTCCACTCCAAAGACCGACTCC 286
Qy 326 ACCCAAGCTTGGCTTCCGATACATCGCGCTCGGAAACGAAAGTCAATCCCGCGCGCCAAAG 385
Db 287 ACCTCCCGAGCTCCGCGCGAGTTGGGCTCTCTCGCTCTCTCTCCAGCCCAACACC 346
Qy 386 CTCAGTAGCTCTCCAGCGATGAACAATACATAGTCCGCGCTCTCTCTCTCGCGCGCTTC 445
Db 347 CCGACTCTCCGACCTCTTTTCGCGGACATCGAGTTCTCCGAGTCGCGACACTCTTCT 406
Qy 446 AGACATCAAGTCTCCACATCAGTCTCTTCGGGCTGTGGTACCTCATATCCCGCT 505
Db 407 CCGAGTCGGGTCAACTCTCTCCCGGCTCTCCCGCTCTATCCCGCGCGGACACTCCCGCC 466
Qy 506 CAGCTGGCTC 515
Db 467 TCGCGGACTC 476

RESULT 7

US-11-052-554A-517
; Sequence 517, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 517
; LENGTH: 9903
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-517

Query Match 4.9%; Score 54.8; DB 14; Length 9903;
Best Local Similarity 50.3%; Pred. No. 7.6e-05;
Matches 162; Conservative 0; Mismatches 157; Indels 3; Gaps 1;
Qy 186 CAGCGCGGACCAAGCCTCTCCAGGGCCTCCAGGGCTCTAAACATCTACCTCATCTCGA 245
Db 8169 CATGCCAACCCGGGCAACCAACACCGGCTGTTCAACATCGGCACCTTCAACACGG 8228
Qy 246 CGTCCCCAATCCGACTTCCAAACATTTGCTCTCGACCAATTCGCGCGCCACCAACTGGGT 305
Db 8229 CATGCCAAACCGGGCCACTACAACACCGGCTCTTAACACCGGTAGTACAACACCGG 8288
Qy 306 CCAAAACCAAGTCCAAAGCTTACCCAAAGTTGCTTCCGATACATCGCCGTCGGAAGCA 365
Db 8289 CATGCCAAACCGCGAGACTACGCGCACCGGCGCTTTCATCACCGGAGCATGAACACGG 8348
Qy 366 AGTCATCCCGCGCGCCAGCTCAGTACGCTCTCCAGCCATGAACACATACAGTCCGC 425
Db 8349 CTTCCTCTGGCGCGCGGAGCGGCTGCTGGCGGCAACTACCATCACCATCGA 8408
Qy 426 CCTCTCTCTGCGGCGCT---TCAGAACATCAAGGTCTCCACATCAGTCTCTCTGGGCT 482
Db 8409 GCGACCTGCGCGCTTCTCAATGTGACATCCCGGTCAACATCCCATCACCGGCGCAT 8468
Qy 483 CGTCGGTACCTCATATCCCCC 504
Db 8469 CACCAATGTCTCCATCCCCGCC 8490

RESULT 8

US-11-138-987-16/c
; Sequence 16, Application US/11138987
; Publication No. US20050278800A1
; GENERAL INFORMATION:
; APPLICANT: Elton, Claire K
; APPLICANT: Hall, Claire
; APPLICANT: Demmer, Jeroen
; TITLE OF INVENTION: Compositions and methods for the modification of
; FILE REFERENCE: 11001.1086U
; CURRENT APPLICATION NUMBER: US/11/138,987
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 60/580,007
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1501

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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-138-987-16

Query Match
Best Local Similarity 4.4%; Score 49.6; DB 14; Length 1501;
Matches 213; Conservative 0; Mismatches 229; Indels 6; Gaps 2;

QY 493 TCATATCCCCCTCAGCTGGCTCTTCTTCCGATGCAATCGTGCATTTGGGTCCAATC 552
Db 580 TCTGGTCGACCTCTCTTCAGGACACTTTAGGGCTGACCTCAACAAGACGATGATTGAATC 521
QY 553 ATACAGTTTCTAGCCAGCAATGGTCCCACTTACTTGCACATCTACCCCTACTTTGAGC 612
Db 520 CTCTCTTTCTCACAAGCACCACCTCTCTCTTTTGTGCAATCTCTCTTTCTCTAAGC 461
QY 613 TATGCTGGCACTCCGGATCCATCGACCTCTCATAGCCCTCTTACTGCAATCTGATACA 672
Db 460 T---TTCACGAAACAGNACATCTCCCTTGACTTTAGGCTCTTTAAAGAAACAGCAAAG 404
QY 673 GTCGTACAGGCGGTCTTACGCTTACAAACACCTCTTTCGATGCCATGGTCGACGATTG 732
Db 403 GCTCACAAGACGGACGTAAACCTTACAGAAACAGCTTTGATCTAAGCTATGACACACTT 344
QY 733 TACTCGGCTGAGAGCGCGGAGCGGCGGATGTCCTTGTGCTGTGCGAGAGTGCG 792
Db 343 GTCTCTGCAATTGTTCACAATTGGGTTTTTCGGAGGTGGATATCGTTGTCTCAAGATCGGT 284
QY 793 TGGCGCTCAGCGGGGGGACGCGGCGGCTCTAATGCGCAGCTTACAATTTCCAAT 852
Db 283 TGGCTACAGATGAGAGGAAATGCAATCACTGCTGTGAGGCGTCTTTTAAAGGA 224
QY 853 TTGATCAACATGTTGGGTGAGGGGAGCGCGGAGAGGCGGAGGCGCA---TTGAGACCTTAC 909
Db 223 CTGATAGTCTTCTGAGAAAGAGCGCTCTCTCCCGGCTCTCTCTGTTGTAACCTTAC 164
QY 910 ATATTGGCATGTTCAACGAGATCAGA 937
Db 163 ATTGAAGTCTCTTGGACGAGATCAGA 136

RESULT 9
US-11-128-061-426
; Sequence 426, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426
; LENGTH: 6645
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4002)..(4019)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-426

Query Match
Best Local Similarity 4.3%; Score 48.2; DB 14; Length 6645;
Matches 204; Conservative 24; Mismatches 252; Indels 9; Gaps 1;

QY 113 GTGCAACCTCCCGCAGCCCGCGAGGTGGTCACTCTACAGTCCCAACACATAGCTG 172
Db 5121 GAGCCACGCTCCCGCGGGGCTATACACCCAGAGCCCTTCATCTCTCTTACTTCCAC 5180
QY 173 GCATCGAGCTCTACAGCCCGCAAGCCACTCTCCAGGCCCTCCAGGCTCTTAACATCT 232
Db 5181 TCCTACTCCCAACTCTCGCCATCTTATTCGCCACAGTCCCACTATAGCCCTACRICA 5240
QY 233 ACCTCATCTCGAGTCTCCCAACTCCGACCTCCAAAACATTCGCTCCGACCAATCGCG 292
Db 5241 CTTAGCTACTCKCCRACTCTCCATCTCTCTSCCAACTCTCTCWWSTACTCTCWCRCACC 5300
QY 293 CCACCACTGGTCCAAACCAAGCTCCAGCTTACCCAAAGTTCGCTTCGGATACATCG 352
Db 5301 TCTCATCTCTCTCCCRACCTCTCTCCAGCTTCTCCCRACCTCTCTCTCTCTCTCTCT 5360
QY 353 CCGTCGAAACGAAGTCAATCCCGCGGCGCAAGCTCAGTAGCTCTCCAGCCATGAACA 412
Db 5361 ACATCACCAGTACTCTCCCRACCTCTCTCCAGC-----TACTCCCRACATCWCY 5411
QY 413 ACATACAGTCCGCTCTCTCTCTGCGGCTTTCAAGACATCAAGGTCTCCACATCAGTCT 472
Db 5412 AGTACTCACCMACTCTCCAGCTTCTCCAGCTTCTCCGMACTTCCCAAGTATCTCTCCACCTCC 5471
QY 473 CTTGCGGCTGTCGGTACTCATATCCCGCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 532
Db 5472 CCCAGTACTCACCAGCTCTCCAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5531
QY 533 CGTGCACTTGGTCCCAATCATATAGTCTTCTAGCCAGCAATGGCTCCCACTTACTTTGCCA 592
Db 5532 TCTCAAGTATTTCWCCACACGCGCTTAATTTCTCCACTAGTCCCAATTAYACSCCA 5591
QY 593 ACATCTACC 601
Db 5592 ACATCMCCC 5600

RESULT 10
US-11-128-049-426
; Sequence 426, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 426
; LENGTH: 6645
; TYPE: DNA
; ORGANISM: Cricetulus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4002)..(4019)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-426
```


QY 476 TCGCGCTCGTACCTCATATCCCCCTCAGCTGGCTCTTCTTCCGA 527
Db 826 TCTACAACCTTCAACAACCTCTACCACTTCTACCGCTCCCAAGA 877

RESULT 13

US-11-205-109-1
; Sequence 1, Application US/11205109
; Publication NO. US20050287641A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Staffa, Alfredo
; TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
; FILE REFERENCE: 3002-2US
; CURRENT APPLICATION NUMBER: US/11/205,109
; CURRENT FILING DATE: 2005-08-17
; PRIOR APPLICATION NUMBER: US/09/976,059
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/239,924
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; NAME/KEY: misc feature
; LOCATION: (2077)..(3078)
; OTHER INFORMATION: ORF 1; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3118)..(4032)
; OTHER INFORMATION: ORF 2; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6665)..(5814)
; OTHER INFORMATION: ORF 4; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7703)..(6693)
; OTHER INFORMATION: ORF 5; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9464)..(8130)
; OTHER INFORMATION: ORF 6; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9691)..(10761)
; OTHER INFORMATION: ORF 7; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12751)..(10829)
; OTHER INFORMATION: ORF 8; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13617)..(12802)
; OTHER INFORMATION: ORF 9; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15203)..(13614)
; OTHER INFORMATION: ORF 10; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15591)..(15863)
; OTHER INFORMATION: ORF 11; positive strandedness
; FEATURE:
; NAME/KEY: misc feature

; LOCATION: (15880)..(19035)
; OTHER INFORMATION: ORF 12; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19032)..(39713)
; OTHER INFORMATION: ORF 13; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (39713)..(65800)
; OTHER INFORMATION: ORF 14; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65826)..(66530)
; OTHER INFORMATION: ORF 15; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66546)..(67370)
; OTHER INFORMATION: ORF 16; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67384)..(70059)
; OTHER INFORMATION: ORF 17; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70059)..(70662)
; OTHER INFORMATION: ORF 18; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70859)..(71906)
; OTHER INFORMATION: ORF 19; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (73439)..(71964)
; OTHER INFORMATION: ORF 20; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (74216)..(73563)
; OTHER INFORMATION: ORF 21; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (75424)..(74213)
; OTHER INFORMATION: ORF 22; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (75535)..(76464)
; OTHER INFORMATION: ORF 23; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (78110)..(76449)
; OTHER INFORMATION: ORF 24; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (79864)..(78107)
; OTHER INFORMATION: ORF 25; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81624)..(79861)
; OTHER INFORMATION: ORF 26; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81909)..(81682)
; OTHER INFORMATION: ORF 27; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82346)..(82062)
; OTHER INFORMATION: ORF 28; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82587)..(84446)
; OTHER INFORMATION: ORF 29; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (84481)..(85548)

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; OTHER INFORMATION: ORF 30; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85556)..(86845)
; OTHER INFORMATION: ORF 31; positive strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87372)..(86803)
; OTHER INFORMATION: ORF 32; negative strandedness
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (87494)..(88420)
; OTHER INFORMATION: ORF 33; positive strandedness; N-terminus only
US-11-205-109-1

Query Match          4.2%; Score 47.2; DB 14; Length 88421;
Best Local Similarity 46.6%; Pred. No. 0.028;
Matches 151; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 115 GACAACTCCCGCAGCGCGGACGCTGCTCAACTCTTAAAGTCCAAACAATAGCTGGC 174
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52991 GCCGACCAACCCCGTCCGCGGAGGCCACCTACCGCGGCCACACCGTGGAGTTACCCGTG 53050

Qy 175 ATGGCACTCTACAGCCCGGACCAAGCCACTCTCCAGGCCCTCCAGGGCTCTAAACATCTAC 234
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53051 CCCCAGCGGTGTCACCACTCGCGAACTCGCGCCCGGAAAGCGGCTCACCGTCTTC 53110

Qy 235 CTCATCTCGAGTCCCAACTCCGACCTCCAAACATTGGCTCCGACCAATCCGCGGCC 294
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53111 ATGACCGTGCAACCGCCTCGCGTCTCTGTCCAACTCGGCGCGGACCGACATC 53170

Qy 295 ACCAACTGGTCCAAACCAAGTCCAGCGCTACCCAAAGTGTGCTTCGGATACATCGCC 354
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53171 CCCATCGCGTGGCGTGGCGGAGCGACCGACCCACCTCGACCAACTCATCGGCTTC 53230

Qy 355 GTCGAAACGAAGTATCCCGGGCGCAAGCTCAGTACGTCTCCAGCCATGAACAAC 414
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53231 TTCGTCAACACCTCGTCTGACACCGACTGACCGGCAACCCACCATCACCGACCTG 53290

Qy 415 ATACAGTCCGCGCTCTCTCTGCC 438
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
53291 CTGACCGCACCCGCGACACCAACC 53314
```

```
RESULT 14
US-11-121-086-42
; Sequence 42, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 142303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-42

Query Match          4.2%; Score 47; DB 14; Length 142303;
Best Local Similarity 48.0%; Pred. No. 0.039;
Matches 134; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 97 TGCATGGAATGGAGCGTGACAACCTCCCGCGCGCGAGCGTGGTCAACCTCTTACAAG 156
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22547 TACAACCCCATCCCGTCTCCATCATGTACAAACCCCACTCCCACTCCATCGTGTACAA 22606
```

```
Qy 157 TCGAACAACTAGCTGGCATCGGACTCTACAGCCCGGACCAAGCACTCTCCAGGCCCTC 216
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22607 CCCATCCCGCTTCCATCACTACAGTACAGCCCATCCCACTCCATCACAATACCAACCCCATC 22666

Qy 217 CAGGGCTCTAACTCTACCTCATCTCGAGCTGCCCAACTCCGACCTCCAAAACATTGCC 276
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22667 CCTATCTCTATCATGTACAGCCCATCCACATCTCCATCACAATCAACCTCATCCCTATC 22726

Qy 277 TCCGACCAATCCGCGGCCACCAACTGGGTCAAAACCAAGTCCAAAGCTTACCCAAACGTT 336
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22727 TCCATCATATACAACTCCATCTCTCCAAAACATACAACCCCATCCCACTCCCATC 22786

Qy 337 GCCTTCCGATACATCGCGTGGGAAACGAAGTCAATCCCC 375
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22787 ACATAACAACCCATCCCACTCCATCACAATGCAACCCCC 22825

RESULT 15
US-11-114-798-52
; Sequence 52, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 165911
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-52

Query Match          4.2%; Score 47; DB 11; Length 165911;
Best Local Similarity 48.0%; Pred. No. 0.042;
Matches 134; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 97 TGCATGGAATGGAGCGTGACAACTCCCGCGCGCGAGCGTGGTCAACCTCTTACAAG 156
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131525 TACAACCCCATCCCGCTCTCCATCATGTACAAACCCCATCCCACTCCATCGTGTACAA 131584

Qy 157 TCCAAACAATAGCTGGCATCGGACTCTACAGCCCGGACCAAGCACTCTCCAGGCCCTC 216
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131585 CCGATCCCGCTTCCATCAGTACAGTACACCCCATCCCACTCCATCACAATACCAACCCCATC 131644

Qy 217 CAGGGCTCTAACTCTACCTCATCTCGAGCTGCCCAACTCCGACCTCCAAAACATTGCC 276
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131645 CCTATCTCTATCATGTACAAACCCCATCCACATCTCCATCACAATCAACCTCATCCCTATC 131704

Qy 277 TCCGACCAATCCGCGGCCACCAACTGGGTCAAAACCAAGTCCAAAGCTTACCCAAACGTT 336
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131705 TCCATCATATACAACTCCATCTCTCCAAAACATACAACCCCATCCCACTCCCATC 131764

Qy 337 GCCTTCCGATACATCGCGTGGGAAACGAAGTCAATCCCC 375
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
131765 ACATAACAACCCATCCCACTCCATCACAATGCAACCCCC 131803
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Search completed: April 7, 2006, 22:54:12
Job time : 664 secs